

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 26, 2003, 12:17:06 ; Search time 350 Seconds
(without alignments)
8975.822 Million cell updates/sec

Title: US-09-828-592-6

Perfect score: 1395

Sequence: 1 atgattccatgtagtag.....ccaaccctgtgtaagtaa 1395

Scoring table:

IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

N.Geneseq_101002:*
1: /SID82/gcgdata/geneeq/geneeqn-emb1/NA1980.DAT:*
2: /SID82/gcgdata/geneeq/geneeqn-emb1/NA1981.DAT:*
3: /SID82/gcgdata/geneeq/geneeqn-emb1/NA1982.DAT:*
4: /SID82/gcgdata/geneeq/geneeqn-emb1/NA1983.DAT:*
5: /SID82/gcgdata/geneeq/geneeqn-emb1/NA1984.DAT:*
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21: /SID82/gcgdata/geneeq/geneeqn-emb1/NA2000.DAT:*
22: /SID82/gcgdata/geneeq/geneeqn-emb1/NA2001A.DAT:*
23: /SID82/gcgdata/geneeq/geneeqn-emb1/NA2001B.DAT:*
24: /SID82/gcgdata/geneeq/geneeqn-emb1/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1395	100.0	1355	24	ABK13828
2	1393.4	99.9	1489	12	AAQ10323
3	1391.8	99.8	1525	21	AAZ29808
4	1391.8	99.8	1599	22	AAZ54046
5	1390.2	99.7	1599	4	AAQ50415
6	1388.6	99.5	1395	14	AAQ50415
7	1387	99.4	1444	22	AAZ3246
8	1375.6	98.6	1467	20	AAZ32160
9	1295.6	92.9	1382	19	AAV41731

10	1294.2	92.8	1299	19	AAV41727	DNA encoding the m
11	1191.8	85.4	2123	23	AAZ83474	DNA encoding novel
12	512.4	36.7	1724	23	AAZ83475	DNA encoding novel
13	397.4	28.5	578	22	ABA63061	Human foetal liver
14	390.2	28.0	395	22	ABA75533	Human foetal liver
15	340	24.4	433	23	AAZ83471	DNA encoding novel
16	323.8	23.2	368	23	AAZ83472	DNA encoding novel
17	267.4	19.2	326	23	AAZ83472	DNA encoding novel
18	254	18.2	355	24	ABN5082	Gene #1580 used to
19	254	18.2	358	16	AAZ20810	Human gene signatu
20	179.8	12.9	238	20	AAZ22166	Human antithrombin
21	139.8	10.0	1492	19	AAV38747	CDNA nESP15-1492 e
22	139.8	10.0	1492	19	AAV38748	Complementary stru
23	132	9.5	1414	19	AAV38745	CDNA nESP14-1414 e
24	132	9.5	1414	19	AAV38746	Complementary stru
25	131	9.4	1393	17	AAZ75221	Cytoplasmic antipr
26	131	9.4	1393	21	AAZ39750	Human cytoplasmic
27	131	9.4	1626	24	ABK84415	Human CDNA differe
28	128.8	9.2	1358	19	AAV38741	CDNA nESP12-1358 e
29	128.8	9.2	1358	19	AAV38742	Complementary stru
30	126.6	9.1	1454	19	AAV38749	CDNA nESP16-1454 e
31	126.6	9.1	1454	19	AAV38750	Complementary stru
32	126.4	9.1	1584	19	AAV38740	Complementary stru
33	126.4	9.1	1584	19	AAV38739	CDNA nESP11-1584 e
34	126.4	9.1	2944	20	AAZ87831	Mouse neuroserpin
35	126.4	9.1	2944	21	AAZ49271	Murine neuroserpin
36	126.2	9.0	1838	19	AAV38743	CDNA nESP13-1838 e
37	126.2	9.0	1838	19	AAV38744	Complementary stru
38	124.6	8.9	1325	24	ABK83894	Human CDNA differe
39	124.6	8.9	1425	21	AAZ39749	Human cytoplasmic antipr
40	124.6	8.9	1425	21	AAZ39749	Human cytoplasmic antipr
41	119	8.5	1316	16	AAO75377	Human elastase inh
42	119	8.5	1316	17	AAZ14255	Human elastase inh
43	119	8.5	1316	24	ABK84121	Human CDNA differe
44	119	8.5	1316	24	ABK69984	Pancreas cancer re
45	119	8.5	1931	21	AAZ77964	Human cancer assoc

ALIGNMENTS

RESULT 1	ABK13828	ABK13828 standard; DNA; 1395 BP.
ID	ABK13828	
AC	ABK13828	
DT	08-MAY-2002 (first entry)	
DE	DNA encoding human antithrombin III (AT3).	
KW	Human, antithrombin III; AT3; H-helix; AT-pos; coagulation deficiency; haemophililia; factor VIII; thrombin; T-TW; anticoagulant; hemostatic; gene; ds.	
KW	Homo sapiens.	
OS	US2001055591-A1.	
FN	27-DEC-2001.	
PD	06-APR-2001; 2001US-0826592.	
PF	07-APR-2000; 2000US-195872P.	
FR	(WALS/) WALSTON T.	
PA	(COOP/) COOPER S.	
PA	(REZA/) REZAEI A.	
XX	Walston T, Cooper S, Rezaei A,	
XX	WPI; 2002-170988/22.	
DR		
XX		

PT Amino acid sequence useful for inhibiting thrombin activity comprises
 PT antithrombin containing an H-helix having an amino acid modified to
 PT have a more positive charge than an H-helix of non-modified
 PT antithrombin -
 PS Disclosure; Page 13; 20pp; English.
 XX
 CC The present invention relates to mutant human antithrombin (AT) having
 CC a modified H-helix to have a more positive charge (AT-pos) than a
 CC H-helix of the wild type antithrombin. The amino acid sequences of
 CC the modified AT H-helices are provided in the specification. The
 CC mutant AT can be used for treating coagulation deficiency in a
 CC patient, for treating haemophilia, and for extending the bioavailability
 CC of factor VIII in a patient. The modified AT modulates the activity of
 CC thrombin, and extends the length of time factor VIII is present in the
 CC blood-stream of the patient and reduces the frequency and/or dosage of
 CC factor VIII infusions needed by the patient. The mutant AT has enhanced
 CC inhibitory activity against the bound form T-TM and thus blocks a
 CC negative feedback loop, resulting in enhanced production of thrombin.
 CC The present sequence represents DNA encoding wild type human
 CC antithrombin III (AT3).
 CC
 SQ Sequence 1395 BP; 366 A; 352 C; 346 G; 331 T; 0 other;
 Query Match 100.0%; Score 1395; DB 24; Length 1395;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1395; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGATATTCAGATGTAGTAACTGTAACCTCTGAAAAAGAGGTTATCTTTGTC 60
 DB 1 ATGATATTCAGATGTAGTAACTGTAACCTCTGAAAAAGAGGTTATCTTTGTC 60
 QY 61 TTGCTGCTCATTTGGCTTTGGGACTGCGTACCGGAGCCCTGTGACATCTGC 120
 DB 61 TTGCTGCTCATTTGGCTTTGGGACTGCGTACCGGAGCCCTGTGACATCTGC 120
 QY 121 AACAGCCAGCCGGGAGCATTTCCATGATCCCATGTGATTAACGCTCCCGAGAG 180
 DB 121 AACAGCCAGCCGGGAGCATTTCCATGATCCCATGTGATTAACGCTCCCGAGAG 180
 QY 181 AAGGCACTGAGGATGAGGCTCAGAAAGAGATCCGAGGAGCCCAACCGGCGTGC 240
 DB 181 AAGGCACTGAGGATGAGGCTCAGAAAGAGATCCGAGGAGCCCAACCGGCGTGC 240
 QY 241 TGGGAATCTGCAAGGCAATTCCTGCTTCTACCACTTTATCAGACCTGCGAGAT 300
 DB 241 TGGGAATCTGCAAGGCAATTCCTGCTTCTACCACTTTATCAGACCTGCGAGAT 300
 QY 301 TCCAGAAATGACATGATTAACATTTTCTGTCAACCTGAGATCTCCAGGCTTTGCT 360
 DB 301 TCCAGAAATGACATGATTAACATTTTCTGTCAACCTGAGATCTCCAGGCTTTGCT 360
 QY 361 ATGACCAAGCTGGGCTCTGTATGACACCTCCAGCAACTGATGAGGATTTAGTT 420
 DB 361 ATGACCAAGCTGGGCTCTGTATGACACCTCCAGCAACTGATGAGGATTTAGTT 420
 QY 421 GACACCAATCTGAGAAAACATCTGATCAGATCACTTCTTCCAACTGAACTGC 480
 DB 421 GACACCAATCTGAGAAAACATCTGATCAGATCACTTCTTCCAACTGAACTGC 480
 QY 481 CGACTCTATCGAAAACCAAAATCTCCAAATTTAGTATGAGCAATGCGCTTTTGA 540
 DB 481 CGACTCTATCGAAAACCAAAATCTCCAAATTTAGTATGAGCAATGCGCTTTTGA 540
 QY 541 GACAAATCCCTTACCTTCAATGAGACTTCAAGACATCATGATGATGATGAGCC 600
 DB 541 GACAAATCCCTTACCTTCAATGAGACTTCAAGACATCATGATGATGATGAGCC 600
 QY 601 AAGCTCAGCCCTTGAGCTTCAAGAAAATGAGAGCAATTCAGAGCGGCATCAACA 660
 DB 601 AAGCTCAGCCCTTGAGCTTCAAGAAAATGAGAGCAATTCAGAGCGGCATCAACA 660
 QY 661 TGGGTGTCCAAATAGACCGAAGCGCAATCAACGATGTCAATCCCTCGGAAGCAAT 720

DB 661 TGGGTGTCCAAATAGACCGAAGCGCAATCAACGATGTCAATCCCTCGGAAGCAAT 720
 QY 721 GAGCTCACTGTTCTGGTCTGGTTAAACACATTTACTTCAAGAGGCTGTGAACTCAAG 780
 DB 721 GAGCTCACTGTTCTGGTCTGGTTAAACACATTTACTTCAAGAGGCTGTGAACTCAAG 780
 QY 781 TTACAGCCCTGAGAACACAGAGAACTGTTCTTCAAGAGCTGATGAGAGTCTGTTCA 840
 DB 781 TTACAGCCCTGAGAACACAGAGAACTGTTCTTCAAGAGCTGATGAGAGTCTGTTCA 840
 QY 841 GCATCTATGATGTACAGAGAGGCAAGTCCGTTATCGGCGGTGAGAGCCCAAG 900
 DB 841 GCATCTATGATGTACAGAGAGGCAAGTCCGTTATCGGCGGTGAGAGCCCAAG 900
 QY 901 GTGCTTGAAGTTCCTTCAAGAGTATGATCAATGATGATGATGATGATGATGATGAT 960
 DB 901 GTGCTTGAAGTTCCTTCAAGAGTATGATCAATGATGATGATGATGATGATGATGAT 960
 QY 961 GAGAAAGCTGGCCAGAGTGAAGAGAACTACCCAGAGTCTGAGAGAGTGGCTG 1020
 DB 961 GAGAAAGCTGGCCAGAGTGAAGAGAACTACCCAGAGTCTGAGAGAGTGGCTG 1020
 QY 1021 GATGATTTGAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1080
 DB 1021 GATGATTTGAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1080
 QY 1081 TTCAGTTTGAAGAGACAGCTGCAAGATGATGATGATGATGATGATGATGATGATGAT 1140
 DB 1081 TTCAGTTTGAAGAGACAGCTGCAAGATGATGATGATGATGATGATGATGATGATGAT 1140
 QY 1141 TCCAACTCCAGATTTGTTGAGAGAGGCGATGATGATGATGATGATGATGATGATGAT 1200
 DB 1141 TCCAACTCCAGATTTGTTGAGAGAGGCGATGATGATGATGATGATGATGATGATGAT 1200
 QY 1201 CATTAAGGATTTCTGAGATTAATGAGAGAGGAGTGAAGAGAGTGAAGAGTGAAGAG 1260
 DB 1201 CATTAAGGATTTCTGAGATTAATGAGAGAGGAGTGAAGAGAGTGAAGAGTGAAGAG 1260
 QY 1261 GTGATTTGCTGCGCTTCTGCTAAACCCCAAGGCTGATCTTCAAGAGGAGGCTTTC 1320
 DB 1261 GTGATTTGCTGCGCTTCTGCTAAACCCCAAGGCTGATCTTCAAGAGGAGGCTTTC 1320
 QY 1321 CTGATTTTATTAAGAGAGTCTCTGAAACATATTATCTTCAATGAGGAGATGACCAAC 1380
 DB 1321 CTGATTTTATTAAGAGAGTCTCTGAAACATATTATCTTCAATGAGGAGATGACCAAC 1380
 QY 1381 CCTGTGTTAAGTAA 1395
 DB 1381 CCTGTGTTAAGTAA 1395

RESULT 2
 ID AAQ10323 strand: cdna; 1489 BP.
 XX AAQ10323;
 XX
 AC AAQ10323;
 XX
 DT 10-APR-1991 (first entry)
 XX
 DE Antithrombin III cDNA sequence.
 XX
 KW antithrombin 3; P-region variants; heparin-dependent; Factor Ila;
 KW Factor Xa; meizothrombin; blood coagulation; ss.
 XX
 XX
 FH Key
 FT CDS Location/Qualifiers
 FT 11..1395
 FT /tag= a
 FT /product= mature antithrombin III
 FT 1059..1059
 FT /tag= b
 FT /note= "Book et al, Nucl. Acids. Res 10, 8113, 1982"
 FT 1327..1327
 FT conflict

1. 2. 3. 4. 5. 6. 7. 8. 9. 10. 11. 12. 13. 14. 15. 16. 17. 18. 19. 20. 21. 22. 23. 24. 25. 26. 27. 28. 29. 30. 31. 32. 33. 34. 35. 36. 37. 38. 39. 40. 41. 42. 43. 44. 45. 46. 47. 48. 49. 50. 51. 52. 53. 54. 55. 56. 57. 58. 59. 60. 61. 62. 63. 64. 65. 66. 67. 68. 69. 70. 71. 72. 73. 74. 75. 76. 77. 78. 79. 80. 81. 82. 83. 84. 85. 86. 87. 88. 89. 90. 91. 92. 93. 94. 95. 96. 97. 98. 99. 100. 101. 102. 103. 104. 105. 106. 107. 108. 109. 110. 111. 112. 113. 114. 115. 116. 117. 118. 119. 120. 121. 122. 123. 124. 125. 126. 127. 128. 129. 130. 131. 132. 133. 134. 135. 136. 137. 138. 139. 140. 141. 142. 143. 144. 145. 146. 147. 148. 149. 150. 151. 152. 153. 154. 155. 156. 157. 158. 159. 160. 161. 162. 163. 164. 165. 166. 167. 168. 169. 170. 171. 172. 173. 174. 175. 176. 177. 178. 179. 180. 181. 182. 183. 184. 185. 186. 187. 188. 189. 190. 191. 192. 193. 194. 195. 196. 197. 198. 199. 200. 201. 202. 203. 204. 205. 206. 207. 208. 209. 210. 211. 212. 213. 214. 215. 216. 217. 218. 219. 220. 221. 222. 223. 224. 225. 226. 227. 228. 229. 230. 231. 232. 233. 234. 235. 236. 237. 238. 239. 240. 241. 242. 243. 244. 245. 246. 247. 248. 249. 250. 251. 252. 253. 254. 255. 256. 257. 258. 259. 260. 261. 262. 263. 264. 265. 266. 267. 268. 269. 270. 271. 272. 273. 274. 275. 276. 277. 278. 279. 280. 281. 282. 283. 284. 285. 286. 287. 288. 289. 290. 291. 292. 293. 294. 295. 296. 297. 298. 299. 300. 301. 302. 303. 304. 305. 306. 307. 308. 309. 310. 311. 312. 313. 314. 315. 316. 317. 318. 319. 320. 321. 322. 323. 324. 325. 326. 327. 328. 329. 330. 331. 332. 333. 334. 335. 336. 337. 338. 339. 340. 341. 342. 343. 344. 345. 346. 347. 348. 349. 350. 351. 352. 353. 354. 355. 356. 357. 358. 359. 360. 361. 362. 363. 364. 365. 366. 367. 368. 369. 370. 371. 372. 373. 374. 375. 376. 377. 378. 379. 380. 381. 382. 383. 384. 385. 386. 387. 388. 389. 390. 391. 392. 393. 394. 395. 396. 397. 398. 399. 400. 401. 402. 403. 404. 405. 406. 407. 408. 409. 410. 411. 412. 413. 414. 415. 416. 417. 418. 419. 420. 421. 422. 423. 424. 425. 426. 427. 428. 429. 430. 431. 432. 433. 434. 435. 436. 437. 438. 439. 440. 441. 442. 443. 444. 445. 446. 447. 448. 449. 450. 451. 452. 453. 454. 455. 456. 457. 458. 459. 460. 461. 462. 463. 464. 465. 466. 467. 468. 469. 470. 471. 472. 473. 474. 475. 476. 477. 478. 479. 480. 481. 482. 483. 484. 485. 486. 487. 488. 489. 490. 491. 492. 493. 494. 495. 496. 497. 498. 499. 500. 501. 502. 503. 504. 505. 506. 507. 508. 509. 510. 511. 512. 513. 514. 515. 516. 517. 518. 519. 520. 521. 522. 523. 524. 525. 526. 527. 528. 529. 530. 531. 532. 533. 534. 535. 536. 537. 538. 539. 540. 541. 542. 543. 544. 545. 546. 547. 548. 549. 550. 551. 552. 553. 554. 555. 556. 557. 558. 559. 560. 561. 562. 563. 564. 565. 566. 567. 568. 569. 570. 571. 572. 573. 574. 575. 576. 577. 578. 579. 580. 581. 582. 583. 584. 585. 586. 587. 588. 589. 590. 591. 592. 593. 594. 595. 596. 597. 598. 599. 600. 601. 602. 603. 604. 605. 606. 607. 608. 609. 610. 611. 612. 613. 614. 615. 616. 617. 618. 619. 620. 621. 622. 623. 624. 625. 626. 627. 628. 629. 630. 631. 632. 633. 634. 635. 636. 637. 638. 639. 640. 641. 642. 643. 644. 645. 646. 647. 648. 649. 650. 651. 652. 653. 654. 655. 656. 657. 658. 659. 660. 661. 662. 663. 664. 665. 666. 667. 668. 669. 670. 671. 672. 673. 674. 675. 676. 677. 678. 679. 680. 681. 682. 683. 684. 685. 686. 687. 688. 689. 690. 691. 692. 693. 694. 695. 696. 697. 698. 699. 700. 701. 702. 703. 704. 705. 706. 707. 708. 709. 710. 711. 712. 713. 714. 715. 716. 717. 718. 719. 720. 721. 722. 723. 724. 725. 726. 727. 728. 729. 730. 731. 732. 733. 734. 735. 736. 737. 738. 739. 740. 741. 742. 743. 744. 745. 746. 747. 748. 749. 750. 751. 752. 753. 754. 755. 756. 757. 758. 759. 760. 761. 762. 763. 764. 765. 766. 767. 768. 769. 770. 771. 772. 773. 774. 775. 776. 777. 778. 779. 780. 781. 782. 783. 784. 785. 786. 787. 788. 789. 790. 791. 792. 793. 794. 795. 796. 797. 798. 799. 800. 801. 802. 803. 804. 805. 806. 807. 808. 809. 810. 811. 812. 813. 814. 815. 816. 817. 818. 819. 820. 821. 822. 823. 824. 825. 826. 827. 828. 829. 830. 831. 832. 833. 834. 835. 836. 837. 838. 839. 840. 84

| Y | 1 | ATCTATTCTCAATGCGGATTTT | 0; mismatches | 1; Indels | 0; Gaps | 0; |
|---|---|------------------------|---------------|-----------|---------|----|
| | | | | | | |

| | | | |
|--|------|--|------|
| Db | 491 | CGACTCTATGAAAAAGCCAAATCCCTCCAGTTAGTATCAGCCATCGCCTTTTGG | 550 |
| Qy | 541 | GACAAATCCCTTACCTTCAATGAGACCTTACCGAGACATAGTGAATTGATATGAGCC | 600 |
| Db | 551 | GACAAATCCCTTACCTTCAATGAGACCTTACCGAGACATAGTGAATTGATATGAGCC | 610 |
| Qy | 601 | AAGCTCCAGCCCTTCGACTTCAAGGAAAATGCAAGCAATCAGAGCGGCATCAACAA | 660 |
| Db | 611 | AGGCTCCAGCCCTTCGACTTCAAGGAAAATGCAAGCAATCAGAGCGGCATCAACAA | 670 |
| Qy | 661 | TGGGTGTCCAATTAAGACCGAAGCCGAATCAACGATGTCATTCCTCTGGAAAGCCAT | 720 |
| Db | 671 | TGGGTGTCCAATTAAGACCGAAGCCGAATCAACGATGTCATTCCTCTGGAAAGCCAT | 730 |
| Qy | 721 | GAGCTCACTGTTCTGGTGTCTGGTTAAACCCATTTATCTTCAAGGAGCCTGTGAAAGTCA | 780 |
| Db | 731 | GAGCTCACTGTTCTGGTGTCTGGTTAAACCCATTTATCTTCAAGGAGCCTGTGAAAGTCA | 790 |
| Qy | 781 | TTGAGCCCTGAGAACACAGAGAGAACTGTTCTACAGAGCTGATGAGAAAGTCGTTC | 840 |
| Db | 791 | TTGAGCCCTGAGAACACAGAGAGAACTGTTCTACAGAGCTGATGAGAAAGTCGTTC | 850 |
| Qy | 841 | GCATCTAGTAGTATCAGAGAGGCAATTCGCTTATCCGCGCGGTGAGAGCACCAG | 900 |
| Db | 851 | GCATCTAGTAGTATCAGAGAGGCAATTCGCTTATCCGCGCGGTGAGAGCACCAG | 910 |
| Qy | 901 | GTGCTTGAGTTGGCCCTTCAAGGTGATGATCATCAATCAGTGTCTGATTTGCCAAAGCT | 960 |
| Db | 911 | GTGCTTGAGTTGGCCCTTCAAGGTGATGATCATCAATCAGTGTCTGATTTGCCAAAGCT | 970 |
| Qy | 961 | GAGAAAGCCTGCGCAAGGTGAGAGAGAACTCACCCGAGAGGTGTCGAGAGTGGCTG | 1020 |
| Db | 971 | GAGAAAGCCTGCGCAAGGTGAGAGAGAACTCACCCGAGAGGTGTCGAGAGTGGCTG | 1030 |
| Qy | 1021 | GATGAATTGAGAGATGATGCTGGTGTGTCACATGCCCCGCTTCGCAATTGAGAGCGC | 1080 |
| Db | 1031 | GATGAATTGAGAGATGATGCTGGTGTGTCACATGCCCCGCTTCGCAATTGAGAGCGC | 1090 |
| Qy | 1081 | TTGAGTTTGAAGAGACAGCTGCGAGACATGAGGCTTGTGATCTGTTCAAGCCCTGAAAG | 1140 |
| Db | 1091 | TTGAGTTTGAAGAGACAGCTGCGAGACATGAGGCTTGTGATCTGTTCAAGCCCTGAAAG | 1150 |
| Qy | 1141 | TTCCAACTCCCAAGGTATTTGTCAGAAAGGCGAGAGTACCTTATGTTCTCAGATCATTC | 1200 |
| Db | 1151 | TTCCAACTCCCAAGGTATTTGTCAGAAAGGCGAGAGTACCTTATGTTCTCAGATCATTC | 1210 |
| Qy | 1201 | CATTAAGGCAATTTCTTGAAGTAAATGAAGAGCAGTGAAGCAGCTGCAAGTACCGCTGT | 1260 |
| Db | 1211 | CATTAAGGCAATTTCTTGAAGTAAATGAAGAGCAGTGAAGCAGCTGCAAGTACCGCTGT | 1270 |
| Qy | 1261 | GTGATGTGTGGCCGTTGGCTTAAACCCCAACAGGCTGACTTCAAGGCCAACAGGCTTTC | 1320 |
| Db | 1271 | GTGATGTGTGGCCGTTGGCTTAAACCCCAACAGGCTGACTTCAAGGCCAACAGGCTTTC | 1330 |
| Qy | 1321 | CTGGTTTTTAAAGAGAACTTCTCGAACAATATATCTTCATGAGCAGAGTGAAGCCAA | 1380 |
| Db | 1331 | CTGGTTTTTAAAGAGAACTTCTCGAACAATATATCTTCATGAGCAGAGTGAAGCCAA | 1390 |
| Qy | 1381 | CCTTGCTGTTAAGTAA 1395 | |
| Db | 1391 | CCTTGCTGTTAAGTAA 1405 | |
| RESULT 3 | | | |
| AA229808 | | | |
| ID AA229808 standard; DNA; 1525 BP. | | | |
| XX AA229808; | | | |
| AC | | | |
| XX | | | |
| 27-MAR-2000 (first entry) | | | |
| DT | | | |
| XX | | | |
| Human antithrombin III DNA related sequence. | | | |
| XX | | | |

| | |
|----------------------------|---|
| KW | Human antithrombin III; modified ATIII; elastase-resistance; |
| KW | IGG activated neutrophil resistant; anti-thrombin activity; heparin; |
| KW | anti-factor Xa activity; blood clotting disorder; sepsis; trauma; stroke; |
| KW | thrombin activation-related pathological symptom; restenosis; thrombosis; |
| KW | acute respiratory distress syndrome; thromboembolism; reocclusion; ds. |
| XX | |
| OS | Homu sapiens. |
| XX | |
| PN | MO9958098-A2. |
| XX | |
| PD | 18-NOV-1999. |
| XX | |
| PF | 12-MAY-1999; 99WO-US10549. |
| XX | |
| PR | 12-MAY-1999; 98US-0085197. |
| XX | |
| PR | 05-MAY-1998; 99US-0085197. |
| XX | |
| PA | (BOCK/) BOCK S C. |
| XX | (PICA/) PICARD V. |
| PA | (ZEND/) ZENDEHROUH P. |
| XX | |
| PI | Bock SC, Picard V, Zendehtrouh P; |
| XX | |
| DR | WPI: 2000-116274/10. |
| XX | |
| PT | New modified human antithrombin III compounds, used for treating e.g. |
| PT | sepsis, trauma, acute respiratory distress syndrome, restenosis, |
| PT | thrombosis, thromboembolism or stroke - |
| XX | |
| PS | Disclosure: Pages 71-72; 75pp; English. |
| XX | |
| CC | The present sequence is related to human antithrombin III (ATIII) DNA. |
| CC | Modified ATIIIs have improved resistance to elastase and IGG-activated |
| CC | neutrophils while retain anti-thrombin and anti-factor Xa activities. |
| CC | They may be expressed as glycoforms with enhanced heparin affinity which |
| CC | target the blood vessel wall more efficiently than ATIIIs with normal |
| CC | heparin affinity. Modified ATIII can be used to treat thrombin |
| CC | activation-related pathological symptoms due to sepsis, trauma, acute |
| CC | respiratory distress syndrome, restenosis, thrombosis, thromboembolism |
| CC | and stroke. It can also be used to reduce the risk of reocclusion |
| CC | and restenosis in percutaneous transluminal coronary angioplasty, |
| CC | thrombosis associated with surgery, ischemia/reperfusion injury, and |
| CC | coagulation abnormalities in cancer or surgical patients. |
| CC | Note: there is no specific information about this sequence in the |
| CC | specification. |
| XX | |
| SQ | Sequence 1525 BP; 402 A; 385 C; 364 G; 374 T; 0 other; |
| XX | |
| Query Match | 99.8%; Score 1391.8; DB 21; Length 1525; |
| Best Local Similarity | 99.9%; Pred. No. 0; |
| Matches 1933; Conservative | 0; Mismatches 2; Indels 0; Gaps 0 |
| QY | 1 ATGTATTCGAATGTGATAGAACTGTAACTCTGCAAAAAGAAAGTTATCTTTGTGC 60 |
| DB | 47 ATGTATTCGAATGTGATAGAACTGTAACTCTGCAAAAAGAAAGTTATCTTTGTGC 106 |
| QY | 61 TTGCTGCTCATTTGGCTCTTGTGGAGTCGCGAGCTGTCAAGGAGCCCTGTGACATCTGC 120 |
| DB | 107 TTGCTGCTCATTTGGCTCTTGTGGAGTCGCGAGCTGTCAAGGAGCCCTGTGACATCTGC 166 |
| QY | 121 ACAGCGAAGCCGCGGAGCAATTCCTCCATGATTCCTGATTTACCGCTCCCGGAGAG 180 |
| DB | 167 ACAGCGAAGCCGCGGAGCAATTCCTCCATGATTCCTGATTTACCGCTCCCGGAGAG 226 |
| QY | 181 AAGCGAAGCTGAGAGTGGGCTCAGAAACAGAAAGATCCGAGAGCCCAACCGGCGTGC 240 |
| DB | 227 AAGCGAAGCTGAGAGTGGGCTCAGAAACAGAAAGATCCGAGAGCCCAACCGGCGTGC 286 |
| QY | 241 TGGGAACGTGCCAAGGCCAATTCCTGCTTGTGACCACTTTGATAGACCGGAGAGT 300 |
| DB | 287 TGGGAACGTGCCAAGGCCAATTCCTGCTTGTGACCACTTTGATAGACCGGAGAGT 346 |
| QY | 301 TCCAGAAATGACATGATTAACATTTTCTGTCAACCCCTAGATATCTCAAGGCTTTTGTCT 360 |

[illegible]

| | | | |
|----------|---|-------------------------|------|
| DB | 1427 | CCTTGCTTAAGTAA | 1441 |
| RESULT 4 | | | |
| AAFS4046 | | | |
| ID | AAFS4046 | standard; DNA; 1599 BP. | |
| XX | | | |
| AC | AAFS4046; | | |
| XX | | | |
| DT | 30-MAR-2001 | (first entry) | |
| XX | | | |
| DE | Human antithrombin III DNA, SEQ ID NO:43. | | |
| KM | | | |
| KM | Age-related gene regulation; gene expression; human protein C; hPC; | | |
| KM | 5' UTR; 5' untranslated region; age-regulatable expression construct; | | |
| KM | PEA-3 element; polyoma virus activator 3; antisense therapy; | | |
| KM | gene therapy; thrombosis; cardiovascular disease; diabetes; | | |
| KM | Alzheimer's disease; Parkinson's disease; cancer; osteoporosis; | | |
| KM | osteoarthritis; dementia; db. | | |
| XX | | | |
| OS | Homo sapiens. | | |
| XX | | | |
| PN | MO200075279-A2. | | |
| XX | | | |
| PD | 14-DEC-2000. | | |
| XX | | | |
| PF | 06-JUN-2000; 2000WO-US15728. | | |
| XX | | | |
| PR | 09-JUN-1999; 99US-0328925. | | |
| XX | | | |
| PA | (UNMT) UNIV MICHIGAN. | | |
| PI | Kurachi K, Kurachi S; | | |
| DR | WPI; 2001-061708/07. | | |
| PT | New regulatory elements that control age-related gene expression, | | |
| PT | useful in gene therapy and for reducing factor IX expression - | | |
| XX | | | |
| P5 | Disclosure; Fig 11; 225pp; English. | | |
| XX | | | |
| CC | The invention relates to nucleic acid sequences which regulate gene | | |
| CC | expression in an age-related manner and/or in a liver-specific manner. | | |
| CC | The invention identifies regions of the human factor IX (hFIX) gene, and | | |
| CC | a region of the human protein C (hPC) gene, which are age-related | | |
| CC | regulatory sequences. The hFIX age-related regulatory sequences are | | |
| CC | designated AES' (AAFS4016) and AES' (AAFS4017) and are found in the 5' | | |
| CC | UTR (at position 2164-2165 of AAFS4018) and 3' UTR (at position | | |
| CC | 34383-35655 of AAFS4018) respectively. These elements act synergistically | | |
| CC | to increase hFIX levels over the lifespan of an individual; however, they | | |
| CC | can independently exert effects on hFIX mRNA in an age-related manner, | | |
| CC | with AES' acting to stabilise hFIX mRNA, and AES' acting to increase hFIX | | |
| CC | mRNA levels, over time. AES' also directs liver-specific expression. The | | |
| CC | hPC gene age-related regulatory sequence is found in the 5' UTR | | |
| CC | (AAFS4081), and contains two PEA-3 (polyoma virus activator 3) elements | | |
| CC | 5' GAGGAAA-3' and 5' CAGGAA-3'. The age-related regulatory sequences of | | |
| CC | the invention, along with their homologues, variants and fragments, may | | |
| CC | be used in the construction of recombinant expression vectors for the | | |
| CC | expression of a desired sequence in an age-related fashion in a host | | |
| CC | cell. Preferred target genes for expression in such age-regulatable | | |
| CC | expression vectors include those encoding proteins involved in blood | | |
| CC | coagulation (e.g., the pro-coagulants factor IX and factor VIII, and the | | |
| CC | anti-coagulants protein C and antithrombin III), human | | |
| CC | alpha-1-antitrypsin, PEA-3 protein and reporter proteins such as | | |
| CC | luciferase. Preferred promoters for use in such age-regulatable | | |
| CC | expression vectors include the human factor IX promoter, the T7 promoter, | | |
| CC | the T3 promoter and the SP6 promoter. The expression vectors of the | | |
| CC | invention may be used in gene therapy to provide age-related and/or | | |
| CC | liver-specific expression of target genes. Age-regulatable constructs may | | |
| CC | be used in the treatment of such age-related conditions such as | | |
| CC | thrombosis, cardiovascular disease, diabetes, Alzheimer's disease, | | |
| CC | Parkinson's disease, cancer, osteoporosis, osteoarthritis and dementia. | | |
| CC | Specifically, they may be used to express factor IX antisense mRNA in the | | |

| | |
|----------------------------|--|
| CC | treatment of thrombotic conditions associated with the natural |
| CC | age-related rise in factor IX expression. Transgenic cells or animals |
| CC | that contain vectors of the invention are useful as models of these |
| CC | diseases, in screening for potential therapeutic agents and for studying |
| CC | normal processes such as ageing and gene expression. Fragments and |
| CC | homologues of age-related regulatory sequences, are useful as probes to |
| CC | detect, isolate or identify other such sequences in samples. The present |
| CC | sequence represents a nucleic acid sequence which may be incorporated |
| CC | into a vector of the invention. |
| SQ | Sequence 1599 BP; 421 A; 409 C; 375 G; 394 T; 0 other; |
| Query Match | 99.8%; Score 1391.8; DB 22; Length 1599; |
| Best Local Similarity | 99.9%; Pred. No. 0; |
| Matches 1393; Conservative | 0; Mismatches 2; Indels 0; Gaps 0 |
| OY | 1 ATGATTCCTCAATGGATAGTGAACGTAACTCTGTGAAAAAGSAGTTATCTTTGTGCC 60 |
| DB | |
| DB | 121 ATGATTCCTCAATGGATAGTGAACGTAACTCTGTGAAAAAGSAGTTATCTTTGTGCC 180 |
| OY | 61 TTGCTGCTCATTTGGCGTTCTTG6GACTGCCTGACCTTGTCAACGGAGCCTGTGACATCTGC 120 |
| DB | |
| DB | 181 TTGCTGCTCATTTGGCGTTCTTG6GACTGCCTGACCTTGTCAACGGAGCCTGTGACATCTGC 240 |
| OY | 121 ACAGCCAAGCCGCGGAGACATTCCCATGTAATCCCAGTGTGATTTACCCTCCCCGGAGAAG 180 |
| DB | |
| DB | 241 ACAGCCAAGCCGCGGAGACATTCCCATGTAATCCCAGTGTGATTTACCCTCCCCGGAGAAG 300 |
| OY | 181 AAGGCAATGAGAGATGAGGGCTCGAAGAAAGATCCGGAGGCCAACCAACGGCGCTGTC 240 |
| DB | |
| DB | 301 AAGGCAATGAGAGATGAGGGCTCGAAGAAAGATCCGGAGGCCAACCAACGGCGCTGTC 360 |
| OY | 241 TGCGAACTGTCCAAAGGCCAATTTCCCGTTTGGTACCACTTTCTATCAGACAACCTGGCAGAT 300 |
| DB | |
| DB | 361 TGCGAACTGTCCAAAGGCCAATTTCCCGTTTGGTACCACTTTCTATCAGACAACCTGGCAGAT 420 |
| OY | 301 TCCAAAGATGACAAATGATTAACATTTTCCGTGACCCCTGAGTATCTCCACGGCTTTTGCT 360 |
| DB | |
| DB | 421 TCCAAAGATGACAAATGATTAACATTTTCCGTGACCCCTGAGTATCTCCACGGCTTTTGCT 480 |
| OY | 361 ATGACCAAGCTGGGTGCTCTGTATAAGCACCTTCCAGCACTGATGAGGATATTTAAGTTT 420 |
| DB | |
| DB | 481 ATGACCAAGCTGGGTGCTCTGTATAAGCACCTTCCAGCACTGATGAGGATATTTAAGTTT 540 |
| OY | 421 GACACCAATCTGAGAAAACATCTGATCAGATCCACTTCTTTGGCCAAACCTGAACCTGC 480 |
| DB | |
| DB | 541 GACACCAATCTGAGAAAACATCTGATCAGATCCACTTCTTTGGCCAAACCTGAACCTGC 600 |
| OY | 481 CGACTCTATCGAAAAGCCCAACAAATCTCTCCAAGTTAGTATCAGCCAAATGCCTTTTTGGA 540 |
| DB | |
| DB | 601 CGACTCTATCGAAAAGCCCAACAAATCTCTCCAAGTTAGTATCAGCCAAATGCCTTTTTGGA 660 |
| OY | 541 GACCAATCTCTTACCTTCAATGAGACCTTACCGAGACATCAGTAGTGGTATATGAGGCC 600 |
| DB | |
| DB | 661 GACCAATCTCTTACCTTCAATGAGACCTTACCGAGACATCAGTAGTGGTATATGAGGCC 720 |
| OY | 601 AAGCTCCAGCCCTCGGACCTTCAAGGAAATGAGAGCAATCCAGAGCCGCATCAACAAA 660 |
| DB | |
| DB | 721 AAGCTCCAGCCCTCGGACCTTCAAGGAAATGAGAGCAATCCAGAGCCGCATCAACAAA 780 |
| OY | 661 TGGGTGTCCAAATAGAGACCGAAGGCCGGAATCAACCGATGTCACTTCCCTCGAAGCCATCAAT 720 |
| DB | |
| DB | 781 TGGGTGTCCAAATAGAGACCGAAGGCCGGAATCAACCGATGTCACTTCCCTCGAAGCCATCAAT 840 |
| OY | 721 GAGCTCACTGTTCTGTGCTGGTTAACAACCATTTACTTCAAGGGCCTGTGGAAGTCAAG 780 |
| DB | |
| DB | 841 GAGCTCACTGTTCTGTGCTGGTTAACAACCATTTACTTCAAGGGCCTGTGGAAGTCAAG 900 |
| OY | 781 TTCAGCCCTTGAGAACACAAAGAGGAACCTGTTTCAACAAGGCTGATGAGAAAGTCGTGTTCA 840 |
| DB | |
| DB | 901 TTCAGCCCTTGAGAACACAAAGAGGAACCTGTTTCAACAAGGCTGATGAGAAAGTCGTGTTCA 960 |
| OY | 841 GCATCTATGATGATCCAGAAAGGCAAGTTCGGTTATCGGCGCGTGGCTGAAGGCACCCAG 900 |

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Db      961 GCATCTATATATGACGAGAGGCAAGTCCGTTATCGCGCTGAGGCAACCCAG 1020
Qy      901 GTGCTTGAATGTCCTTCAAGGTGATGATCATCACCATGCTCTTCTTCCCAAGCCT 960
Db      1021 GTGCTTGAATGTCCTTCAAGGTGATGATCATCACCATGCTCTTCTTCCCAAGCCT 1080
Qy      961 GAGAGAGCCTGCGCAAGGTGAGAGAGAACTCACCCCAAGGTGCTGCAAGATGCTG 1020
Db      1081 GAGAGAGCCTGCGCAAGGTGAGAGAGAACTCACCCCAAGGTGCTGCAAGATGCTG 1140
Qy      1021 GATGATTTGAGAGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1080
Db      1141 GATGATTTGAGAGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1200
Qy      1081 TTCACTTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1140
Db      1201 TTCACTTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1260
Qy      1141 TCCAAATCTCCAGGATATGTTGCAAGAGCCGAGATGACCTCTATGCTCAAGATGCA 1200
Db      1261 TCCAAATCTCCAGGATATGTTGCAAGAGCCGAGATGACCTCTATGCTCAAGATGCA 1320
Qy      1201 CATTAAGCATTTCTTCAAGGTAATGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1260
Db      1321 CATTAAGCATTTCTTCAAGGTAATGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1380
Qy      1261 GTGATTTGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1320
Db      1381 GTGATTTGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1440
Qy      1321 CTGGTTTATTAAGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1380
Db      1441 CTGGTTTATTAAGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1500
Qy      1381 CCTGTGTTAAGTAA 1395
Db      1501 CCTGTGTTAAGTAA 1515

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RESULT 5

AA30203
ID AA30203 standard; cDNA; 1599 BP.

AC AA30203;

DT 25-MAY-1992 (first entry)

DE Sequence encoding human antithrombin III (ATIII) from cDNA clones
pA62 and pA68.

KW Thrombosis; therapy; cardiovascular disorders; ss.

OS Homo sapiens.

FT Key location/Qualifiers

FT sig_peptide 121..216

FT mat_peptide 217..1515

FT polyA_signal 1599

FT /tag= c

PN GB2116183-A.

PD 21-SEP-1983.

PF 02-MAR-1983; 83GB-0005786.

PR 30-JUL-1982; 82US-0403600.

PR 03-MAR-1982; 82GB-0006262.

PR 02-MAR-1983; 83GB-0005786.

PR 01-FEB-1985; 85US-0697178.

XX (GETH) GENENTECH INC.
XX PA Bock SC, Lawn RM;
XX PI
XX DR WPI: 1983-766797/38.
XX P-PSDB; MAP30445.
XX
XX Human antithrombin III prod. by genetically modified cells - and
PT corresp. cloning vehicles and expression vectors
XX
XX
PS Disclosure; Fig 2; 14pp; English.

CC pA62 and pA68 are overlapping cDNA clones for ATIII. pA62 is
CC incomplete at the 3' end and pA68 comprises 400 bp from the 3'
CC end, 84 bp 3' untranslated region and a poly(A) tail. Plasmids
CC PAT111-57 and PAT111-J4 (claimed) contain a ligation product (pTA2)
CC of pA62 and pA68 (see AA30203).

SQ Sequence 1599 BP; 421 A; 408 C; 375 G; 395 T; 0 other;

Query Match 99.7%; Score 1390.2; DB 4; Length 1599;

Best Local Similarity 99.8%; Pred. No. 0;
Matches 1392; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy      1 ATGTTTTCATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 60
Db      121 ATGTTTTCATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 180
Qy      61 TTGCTGCTCATTTGCTTCTGCGGAGTGGGAGCTGTCACGGGAGCCCTGTGAGATCTGC 120
Db      181 TTGCTGCTCATTTGCTTCTGCGGAGTGGGAGCTGTCACGGGAGCCCTGTGAGATCTGC 240
Qy      121 ACAGCCAAAGCCGCGGAGATTTCCATGAATCCATGTCATTTACCGCTCCCGAGAG 180
Db      241 ACAGCCAAAGCCGCGGAGATTTCCATGAATCCATGTCATTTACCGCTCCCGAGAG 300
Qy      181 AAGGCACTGAGAGATGAGAGAGGCTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
Db      301 AAGGCACTGAGAGATGAGAGAGGCTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
Qy      241 TGGGAATGTCCTCAAGGCAATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
Db      361 TGGGAATGTCCTCAAGGCAATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
Qy      301 TCCAGAAATGACAAATGATTAATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
Db      421 TCCAGAAATGACAAATGATTAATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
Qy      361 ATGACCAAGTGGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
Db      481 ATGACCAAGTGGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
Qy      421 GACACCATATCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
Db      541 GACACCATATCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 600
Qy      481 CGACTCTATCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
Db      601 CGACTCTATCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660
Qy      541 GACAAATCCCTTAACCTTAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 600
Db      661 GACAAATCCCTTAACCTTAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
Qy      601 AAGCTCCAGCCCTGGAATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660
Db      721 AAGCTCCAGCCCTGGAATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 780
Qy      661 TGGGTGTCATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
Db      781 TGGGTGTCATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 840

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Oy 721 GAGCTCACTGTTCTGTCGCTGTTAAACCACTTACTTCAAGGCGCTGTGAAAGTCAAG 780
Db 841 GAGCTCACTGTTCTGTCGCTGTTAAACCACTTACTTCAAGGCGCTGTGAAAGTCAAG 900
Oy 781 TTCAGCCCTGAGAACACAAAGGAAGAACTGTTCTTAAAGGCTGATGAGAGTCTGTTCA 840
Db 901 TTCAGCCCTGAGAACACAAAGGAAGAACTGTTCTTAAAGGCTGATGAGAGTCTGTTCA 960
Oy 841 GCATCTATGATGATACCAAGGAAGCAAGTCCGTTATCCGCGGTGGCTGAAGGCAAGG 900
Db 961 GCATCTATGATGATACCAAGGAAGCAAGTCCGTTATCCGCGGTGGCTGAAGGCAAGG 1020
Oy 901 GTGCTTGAGTGGCCCTTCAAAAGTATGATGATGATGATGATGATGATGATGATGATGAT 960
Db 1021 GTGCTTGAGTGGCCCTTCAAAAGTATGATGATGATGATGATGATGATGATGATGATGAT 1080
Oy 961 GAGAAAGCCTGGCCCAAGGTGAGAAAGAACTGATCCCAAGAGTCTGCAAGAGTGGCTG 1020
Db 1081 GAGAAAGCCTGGCCCAAGGTGAGAAAGAACTGATCCCAAGAGTCTGCAAGAGTGGCTG 1140
Oy 1021 GATGAATTTGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1080
Db 1141 GATGAATTTGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1200
Oy 1081 TTCAGTTTGAAGAGCAGCTGCAAGACATGAGGCTTTCATGATCTGTCAGCCCTGAAG 1140
Db 1201 TTCAGTTTGAAGAGCAGCTGCAAGACATGAGGCTTTCATGATCTGTCAGCCCTGAAG 1260
Oy 1141 TCCAAAGTCCCAAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1200
Db 1261 TCCAAAGTCCCAAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1320
Oy 1201 CATAGGATTTCTTGAAGTAAATGAAGAGCAGTGAAGAGCAGTGAAGAGTCCCTGTT 1260
Db 1321 CATAGGATTTCTTGAAGTAAATGAAGAGCAGTGAAGAGCAGTGAAGAGTCCCTGTT 1380
Oy 1261 GTGATTTGTCGCGCTTCTGCTAAACCCCAAGAGGATGATGATGATGATGATGATGATGAT 1320
Db 1381 GTGATTTGTCGCGCTTCTGCTAAACCCCAAGAGGATGATGATGATGATGATGATGATGAT 1440
Oy 1321 CTGCTTTTATTAAGAAAGTCTCTGTAACACTATATATCTTCTGAGGAGAGTCAAC 1380
Db 1441 CTGCTTTTATTAAGAAAGTCTCTGTAACACTATATATCTTCTGAGGAGAGTCAAC 1500
Oy 1381 CCTTGTGTTAAGTAA 1395
Db 1501 CCTTGTGTTAAGTAA 1515

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RESULT 6
AA050415
ID AA050415 standard; cDNA; 1395 BP.

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XX AA050415;
XX
XX 13-MAY-1994 (first entry)
XX
DE Human antithrombin III cDNA.
XX
XX AT III; mutant; serine protease inhibitor; serpin; thrombosin;
XX blood coagulation; anticoagulant; site-directed mutagenesis; ds.
XX
OS Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 1..1395
XX FT /*tag= a
XX FT sig_peptide 1..95
XX FT mat_peptide 97..1392
XX FT /*tag= b
XX FT /*tag= c
XX FT /*note= "wild-type"
XX

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PN EP568833-A.
XX 10-NOV-1993.
XX
XX 08-APR-1993; 93EP-0105829.
XX
XX 10-APR-1992; 92JP-0090488.
XX
XX 22-FEB-1993; 93JP-0031855.
XX
XX (EISA) EISA CO LTD.
XX
XX Kato H, Mizui Y, Nagaoka N, Seto T, Suzuki N, Suzuki S;
XX Yoshitake S;
XX MPI. 1993-352985/45.
XX P-PDB; ABR42895.
XX
XX New human antithrombin III mutants of high antithrombin activity
XX in absence of heparin - useful as anticoagulant for treating
XX thrombotic disease
XX
XX Example 1; Page 35-37; 137bp; English.
XX
XX A commercially available human liver cDNA library was screened with
XX a probe corresp. to amino acids 314-322 of AT III. Two positive
XX overlapping clones were obtained. Their inserts were subcloned into
XX pUC18 and the complete AT III coding sequence was obtained by
XX ligating subcloned fragments. The full-length sequence provided the
XX basis for a mutagenesis template; novel mutant AT III molecules were
XX generated by site-directed techniques.
XX
XX Sequence 1395 BP; 368 A; 353 C; 343 G; 331 T; 0 other:
XX
XX Query Match 99.5%; Score 1388.6; DB 14; Length 1395;
XX Best Local Similarity 99.7%; Pred. No. 0;
XX Matches 1391; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
XX
Oy 1 ATGATTTCCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 60
Db 1 ATGATTTCCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 60
Oy 61 TTGCTGCTCATTTGCTTCTGAGACTGCTGATGATGATGATGATGATGATGATGATGATGATGAT 120
Db 61 TTGCTGCTCATTTGCTTCTGAGACTGCTGATGATGATGATGATGATGATGATGATGATGATGAT 120
Oy 121 AAGCCAAAGCCGCGGACATTTCCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 180
Db 121 AAGCCAAAGCCGCGGACATTTCCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 180
Oy 181 AAGGCACTGAGATGAGAGGCTCAGAACAGAAAGATCCCGGAGGCCAAGCCGCGGTGTC 240
Db 181 AAGGCACTGAGATGAGAGGCTCAGAACAGAAAGATCCCGGAGGCCAAGCCGCGGTGTC 240
Oy 241 TGGGAAGTGTCCAAAGGCAATTTCCGCTTCTGACACTTCTATCAGACACTGACAGAT 300
Db 241 TGGGAAGTGTCCAAAGGCAATTTCCGCTTCTGACACTTCTATCAGACACTGACAGAT 300
Oy 301 TCCAAAGATGACATGATTAATTTCTGTCACCCCTGAGATGATGATGATGATGATGATGATGAT 360
Db 301 TCCAAAGATGACATGATTAATTTCTGTCACCCCTGAGATGATGATGATGATGATGATGATGAT 360
Oy 361 ATGACCAAGCTGGGGCTGTTAATGACACCCCTCCAGCAAGTGAATGAGATTTTAAGTTT 420
Db 361 ATGACCAAGCTGGGGCTGTTAATGACACCCCTCCAGCAAGTGAATGAGATTTTAAGTTT 420
Oy 421 GACACCATATCTGAGAAACATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 480
Db 421 GACACCATATCTGAGAAACATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 480
Oy 481 CGACTCTATGCAAAAGCCAAATCTCTCAAGTTAGTATGATGATGATGATGATGATGATGATGAT 540
Db 481 CGACTCTATGCAAAAGCCAAATCTCTCAAGTTAGTATGATGATGATGATGATGATGATGATGAT 540

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QY 541 GACAAATCCCTTACCTTCAATGAGACTTACAGACATCATGAGTTGATATGAGCC 600
 DB 541 GACAAATCCCTTACCTTCAATGAGACTTACAGACATCATGAGTTGATATGAGCC 600
 QY 601 AGCTCCAGCCCTTGAATTTCAAGAAAATGCAAGACATCCAGAGCCCATCAACAA 660
 DB 601 AGCTCCAGCCCTTGAATTTCAAGAAAATGCAAGACATCCAGAGCCCATCAACAA 660
 QY 661 TGGGATGTCATTAAGACCGAGGCGCATCCAGATGATTCCTCCGAAAGCCATCAT 720
 DB 661 TGGGATGTCATTAAGACCGAGGCGCATCCAGATGATTCCTCCGAAAGCCATCAT 720
 QY 721 GAGCTCACTGTTCTGGTGTGTTAAACACATTTACTTCAAGGCGCTGGAAGTCAAG 780
 DB 721 GAGCTCACTGTTCTGGTGTGTTAAACACATTTACTTCAAGGCGCTGGAAGTCAAG 780
 QY 781 TTTCAGCCCTGAGAACCAAGAAAGAACTGTTCTAAGGCTGATGGAAGTCTGTTCA 840
 DB 781 TTTCAGCCCTGAGAACCAAGAAAGAACTGTTCTAAGGCTGATGGAAGTCTGTTCA 840
 QY 841 GCATCATATGATGACAGAGAGCAAGTCCGTTATCGCGCGCTGAAAGCAACCA 900
 DB 841 GCATCATATGATGACAGAGAGCAAGTCCGTTATCGCGCGCTGAAAGCAACCA 900
 QY 901 GTGCTTGAAGTTCCTTCAAGAGTGAATGACATCAACATGATGCTTCCCAAGCT 960
 DB 901 GTGCTTGAAGTTCCTTCAAGAGTGAATGACATCAACATGATGCTTCCCAAGCT 960
 QY 961 GAGAAAGCTGCGCCCAAGTGAAGAAAGAACTCAACCCCAAGAGTGTGAGAGTGGCTG 1020
 DB 961 GAGAAAGCTGCGCCCAAGTGAAGAAAGAACTCAACCCCAAGAGTGTGAGAGTGGCTG 1020
 QY 1021 GATGAATTTGAGAGAGATGATGCTGATGATCAATGATGATGATGATGATGATG 1080
 DB 1021 GATGAATTTGAGAGAGATGATGCTGATGATCAATGATGATGATGATGATGATG 1080
 QY 1081 TTTCAGTTTGAAGAGAGAGTGAAGACATGAGGCTTGTGATGTTTCAAGCTTGA 1140
 DB 1081 TTTCAGTTTGAAGAGAGAGTGAAGACATGAGGCTTGTGATGTTTCAAGCTTGA 1140
 QY 1141 TCCAACTCCCAAGTATGTTGTCAGAAAGCCGAGATGATGATGATGATGATGATG 1200
 DB 1141 TCCAACTCCCAAGTATGTTGTCAGAAAGCCGAGATGATGATGATGATGATGATG 1200
 QY 1201 CATTAAGCAATTTCTTGAAGTAAATGAAGAGAGAGAGAGAGAGAGAGAGAGAG 1260
 DB 1201 CATTAAGCAATTTCTTGAAGTAAATGAAGAGAGAGAGAGAGAGAGAGAGAGAG 1260
 QY 1261 GTGATTTGCTGGCCGTTTCTGTAACCCCAACAGAGGTGATCTTCAAGGCAAC 1320
 DB 1261 GTGATTTGCTGGCCGTTTCTGTAACCCCAACAGAGGTGATCTTCAAGGCAAC 1320
 QY 1321 CTGGTTTTTATTAAGAGAGTCTCTGAAACATATTAATCTTCAAGGCAAGAGTGA 1380
 DB 1321 CTGGTTTTTATTAAGAGAGTCTCTGAAACATATTAATCTTCAAGGCAAGAGTGA 1380
 QY 1381 CCTTGTGTTAAGTAA 1395
 DB 1381 CCTTGTGTTAAGTAA 1395

RESULT 7
 AAC83246
 ID AAC83246 standard; cDNA, 1444 BP.
 AC AAC83246;
 XX
 DT 13-MAR-2001 (first entry)
 XX Human antithrombin III cDNA sequence.
 DE Human antithrombin III; antiangiogenic; angiogenesis inhibitor; anticoagulant;
 XX serine protease; human; ss.
 KW

XX OS Homo sapiens.
 XX PN W020069256-A1.
 XX PD 23-NOV-2000.
 XX PF 12-MAY-2000; 2000MO-US13052.
 XX PR 13-MAY-1999; 99US-0134174.
 XX PA (GENZ) GENZYME TRANSGENICS CORP.
 XX PI Meade H, Bourdon PR;
 XX DR WPI; 2001-024924/03.
 XX DR P-PSDB; AAB37963.
 PT Transgenically produced mutated human antithrombin III having
 PT antithrombin activity, useful for therapeutic and diagnostic
 PS applications -
 XX Disclosure; Fig 1; 45pp; English.
 CC This invention relates to a transgenically produced mutated human
 CC antithrombin II polypeptide. Antithrombin III is a serine protease
 CC inhibitor which inhibits thrombin and activated forms of factors X, VII,
 CC IX, XI, and XII. Antithrombin III has antiangiogenic and anticoagulant
 CC activity. The mutated antithrombin III protein of the invention has uses
 CC in the therapy and diagnosis of disease and conditions involving
 CC angiogenesis. The invention includes methods for making a transgenic
 CC animal that produces the recombinant antithrombin III protein in its
 CC milk. The present sequence represents the human antithrombin III cDNA
 CC sequence.
 SO Sequence 1444 BP; 377 A; 371 C; 353 G; 343 T; 0 other;
 Query Match 99.4%; Score 1387; DB 22; Length 1444;
 Best Local Similarity 99.6%; Pred. No. 0;
 Matches 1390; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 1 ATGTTTCCATATGATGAGAACTGTAACCTTGGAAGAGAGTTTATCTTTGTC 60
 DB 16 ATCTATTCATATGATGAGAACTGTAACCTTGGAAGAGAGTTTATCTTTGTC 75
 QY 61 TTGCTGCTCATTTGCTTGGAGTCTGCTGACCTGTCAAGGAGCCGTGTGACATCTGC 120
 DB 76 TTGCTGCTCATTTGCTTGGAGTCTGCTGACCTGTCAAGGAGCCGTGTGACATCTGC 135
 QY 121 ACAGCCAAAGCCGCGGAGCAATTCCTCATGAAATCCCATGTCATTTACCGTCCCGGAGAG 180
 DB 136 ACAGCCAAAGCCGCGGAGCAATTCCTCATGAAATCCCATGTCATTTACCGTCCCGGAGAG 195
 QY 181 AAGGCACTGAGAGTGAAGGAGCTCAGAACAGAGATCCCGAGAGCCACCAACCGGAGTGC 240
 DB 196 AAGGCACTGAGAGTGAAGGAGCTCAGAACAGAGATCCCGAGAGCCACCAACCGGAGTGC 255
 QY 241 TGGGAATGCTCCAAAGCCCAATTCGCTTGTGTAACCTTTCTATCAGACCTGCGAGAT 300
 DB 256 TGGGAATGCTCCAAAGCCCAATTCGCTTGTGTAACCTTTCTATCAGACCTGCGAGAT 315
 QY 301 TCCAAAGATGACATGATTAATCAATTTCTGTGTATCAACCCCTGAGATATCTCCAGGCTTTGCT 360
 DB 316 TCCAAAGATGACATGATTAATCAATTTCTGTGTATCAACCCCTGAGATATCTCCAGGCTTTGCT 375
 QY 361 ATGACCAAGCTGGGAGCCGTATATGACACCCCTCAGCAACTGATGAGAGGATTTAAGTTT 420
 DB 376 ATGACCAAGCTGGGAGCCGTATATGACACCCCTCAGCAACTGATGAGAGGATTTAAGTTT 435
 QY 421 GACACCATATCTGAGAAAAACATCTGATGATCACTTCTTTGTCGCAAGTGAATCTGC 480
 DB 436 GACACCATATCTGAGAAAAACATCTGATGATCACTTCTTTGTCGCAAGTGAATCTGC 495

| | | | |
|----|------|---|------|
| OY | 418 | TTTGGACACATATCTGAGAAAAACATCTGATCAGATCCACTCTTCTTTGCCAAACTGAAAC | 477 |
| Db | 442 | TTTGGACACATATCTGAGAAAAACATCTGATCAGATCCACTCTTCTTTGCCAAACTGAAAC | 501 |
| OY | 478 | TGCGGACTCTATTCGAAANAGCCAAATCTCTCCAGTTAGTATCAGCCCAATGCGCTTTT | 537 |
| Db | 502 | TGCCCACTCTATTCGAAANAGCCAAATCTCTCCAGTTAGTATCAGCCCAATGCGCTTTT | 561 |
| OY | 538 | GGAGACAATCCCTTAACCTTCATAGACCTACAGACATCAGTGAATGTTGATATAGGA | 597 |
| Db | 562 | GGAGACAATCCCTTAACCTTCATAGACCTACAGACATCAGTGAATGTTGATATAGGA | 621 |
| OY | 598 | GCCAAAGCTCCAGGCGCTTCAAGGAAATGCAAGCAATCCAGAGCGGCATCAAC | 657 |
| Db | 622 | GCCAAAGCTCCAGGCGCTTCAAGGAAATGCAAGCAATCCAGAGCGGCATCAAC | 681 |
| OY | 658 | AAATGGGTGTCGAATPAGACCGAAGGCGGAATCACGATGTGATTTCCCTCGGAAAGCCATC | 717 |
| Db | 682 | AAATGGGTGTCGAATPAGACCGAAGGCGGAATCACGATGTGATTTCCCTCGGAAAGCCATC | 741 |
| OY | 718 | AATGAGCTCATCTGTTCTGCTGTGTTAAACCATTTTACTTCAAGAGGCGTGTGAAGTCA | 777 |
| Db | 742 | AATGAGCTCATCTGTTCTGCTGTGTTAAACCATTTTACTTCAAGAGGCGTGTGAAGTCA | 801 |
| OY | 778 | AAGTTCAACCCCTGAGAAACAAAGGAAGAACTGTCTPACAGGCGTGATGAGAGTCGTGT | 837 |
| Db | 802 | AAGTTCAACCCCTGAGAAACAAAGGAAGAACTGTCTPACAGGCGTGATGAGAGTCGTGT | 861 |
| OY | 838 | TCAGCATCTATGATGTATACCAAGAAAGCAATTCGCTTATCGGCGCGTGTGAAGCAC | 897 |
| Db | 862 | TCAGCATCTATGATGTATACCAAGAAAGCAATTCGCTTATCGGCGCGTGTGAAGCAC | 921 |
| OY | 898 | CAGGCGCTTGAGTTGCGCTTCAAAAGTATGATGACATCACATGATGTCATCTTGCGCCAA | 957 |
| Db | 922 | CAGGCGCTTGAGTTGCGCTTCAAAAGTATGATGACATCACATGATGTCATCTTGCGCCAA | 981 |
| OY | 958 | CCTGGAAGAGGCTTGCCCAAGGTGAGAAAGAACTCACCCAGAGAGTGTCTGACAGAGTGG | 1017 |
| Db | 982 | CCTGGAAGAGGCTTGCCCAAGGTGAGAAAGAACTCACCCAGAGAGTGTCTGACAGAGTGG | 1041 |
| OY | 1018 | CTGATGTAATTGGAGAGATGATGCTGTGGTGGTCCATGAGCCCGCTTCCGAGATTGAGGAC | 1077 |
| Db | 1042 | CTGATGTAATTGGAGAGATGATGCTGTGGTGGTCCATGAGCCCGCTTCCGAGATTGAGGAC | 1101 |
| OY | 1078 | GCGCTTCAGTTTGAAGAGACGCTGCAAGACATGGGCGTTGTGATCTGTTCAAGCGCTGAA | 1137 |
| Db | 1102 | GCGCTTCAGTTTGAAGAGACGCTGCAAGACATGGGCGTTGTGATCTGTTCAAGCGCTGAA | 1161 |
| OY | 1138 | AAGTCCAAATCTCCAGGTATTTGTTCCAGAGGCGGAGATGACTCTATGTCAGATGCA | 1197 |
| Db | 1162 | AAGTCCAAATCTCCAGGTATTTGTTCCAGAGGCGGAGATGACTCTATGTCAGATGCA | 1221 |
| OY | 1198 | TTCCATAAGGCAATTTCTTAGGTAAATGAGAAGGCAAGTGAAGCAGCTGCAAGTACCGCT | 1257 |
| Db | 1222 | TTCCATAAGGCAATTTCTTAGGTAAATGAGAAGGCAAGTGAAGCAGCTGCAAGTACCGCT | 1281 |
| OY | 1258 | GTTGATGATTCGCGCGCTTCCGTAAACCCCAAGGATGACTTTCAAGGCCAACAGGCGCT | 1317 |
| Db | 1282 | GTTGATGATTCGCGCGCTTCCGTAAACCCCAAGGATGACTTTCAAGGCCAACAGGCGCT | 1341 |
| OY | 1318 | TTCTGATTTTATTAAGAAAGTTCCTCTGAACACTATTTATCTTCAATGGGAGATGACC | 1377 |
| Db | 1342 | TTCTGATTTTATTAAGAAAGTTCCTCTGAACACTATTTATCTTCAATGGGAGATGACC | 1401 |
| OY | 1378 | AACTCTTGTTAAAGTAA 1395 | |
| Db | 1402 | AACTCTTGTTAAAGTAA 1419 | |

RESULT 9
AAV41731
ID AAV41731 standard; DNA; 1382 BP.

| Accession | Protein Name | Location/Qualifiers |
|---|---|-----------------------------------|
| AAV41731; | | |
| 20-NOV-1998 | (first entry) | |
| Codon-optimised RAmY3D signal fused to DNA encoding mature ATIII. | | |
| Protein expression; monocotyledon plant cell; | | |
| glycosylated alpha 1-antitrypsin; AAT; glycosylated antithrombin III; | | |
| ATIII; human serum albumin; HSA; subtilisin BPN'; treatment; emphysema; | | |
| antithrombotic; blood replacement; ss. | | |
| Synthetic. | | |
| Homo sapiens. | | |
| Key | Location/Qualifiers | |
| misc_feature | 1..75 | |
| | /*tag= a | |
| | /note= "codon-optimised RAmY3D signal sequence" | |
| misc_feature | 76..1382 | |
| | /*tag= b | |
| | /note= "encodes mature ATIII" | |
| WO9836085-A1. | | |
| 20-AUG-1998. | | |
| 13-FEB-1998; | 98WO-US03068. | |
| 13-FEB-1997; | 97US-0038170. | |
| 13-FEB-1997; | 97US-0037991. | |
| 13-FEB-1997; | 97US-0038168. | |
| 13-FEB-1997; | 97US-0038169. | |
| (PHYT-) APPLIED PHYTOLOGICS INC. | | |
| Rodriguez RL, Sutliff TD; | | |
| WPI; 1998-467179/40. | | |
| Expressing mature, glycosylated proteins in monocotyledonous plant cells - from chimeric gene including signal peptide sequence, specifically therapeutic agents and industrial enzymes | | |
| Disclosure; Page 34 iv; 53pp; English. | | |
| The present sequence encodes a fusion protein of codon-optimised RAmY3D signal sequence/mature antithrombin III (ATIII). The protein is used to exemplify the invention. The specification describes a method for producing mature heterologous protein in monocotyledonous plant cells. The method comprises transforming the cells with a chimeric gene comprising a monocotyledon transcription regulator, inducible either during seed maturation or by adding/removing a small molecule, DNA encoding the heterologous protein, and DNA encoding a signal peptide, with the signal peptide causing secretion of the protein from the cell. Proteins expressed in this manner include mature glycosylated alpha 1-antitrypsin (AAT) with a glycosylation pattern that significantly increases its serum half-life, mature glycosylated antithrombin III (ATIII), mature human serum albumin (HSA) having the native folding pattern as shown by biolindin-binding characteristics, or mature active subtilisin BPN'. These proteins are useful therapeutically (e.g. AAT for treating emphysema, ATIII as antithrombotic and HSA as blood replacement) or as industrial enzymes (BPN' is used in detergents). | | |
| Sequence 1382 BP, 358 A, 370 C, 339 G, 315 T, 0 other; | | |
| Query Match | 92.9%; | Score 1295.6; DB 19; Length 1382; |
| Best Local Similarity | 98.9%; | Pred. No. 0; |
| Matches 1304; Conservative | 0; | Mismatches 14; Indels 0; Gaps 0 |

Query Match 92.8%; Score 1294.2; DB 19; Length 1299;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 1296; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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QY 97 CAGGGAGCCCTGTGACATCTGCACAGCCGCGGGGACATCCCATGATCCCATG 156
   |||
Db 1 CACGGAAGCCCTGTGACATCTGCACAGCCGCGGGGACATCCCATGATCCCATG 60
   |||

QY 157 TGCATTACCGCTCCCGGAGAGAGAGCACTGAGATGAGGGCTCAGAACAGAAATC 216
   |||
Db 61 TGCATTACCGCTCCCGGAGAGAGAGCACTGAGATGAGGGCTCAGAACAGAAATC 120
   |||

QY 217 CCGGAGGCCACCAACCGGCTGTCTGGAACTGTCCAGGCCAATTCGGCTTGTACC 276
   |||
Db 121 CCGGAGGCCACCAACCGGCTGTCTGGAACTGTCCAGGCCAATTCGGCTTGTACC 180
   |||

QY 277 ACTTTCATAGACACCTGGCAGATCCCAAGATGACAAATGATAAATTTTCTGTACCC 336
   |||
Db 181 ACTTTCATAGACACCTGGCAGATCCCAAGATGACAAATGATAAATTTTCTGTACCC 240
   |||

QY 337 CTGAGTATCTCAACGGCTTTGCTATGACCAAGCTGGGTGCTGTATGACACCTCCAG 396
   |||
Db 241 CTGAGTATCTCAACGGCTTTGCTATGACCAAGCTGGGTGCTGTATGACACCTCCAG 300
   |||

QY 397 CAACTGATGAGGTATTAAAGTTTGACACCATATCTGAGAAAACATCTGATCATTCAC 456
   |||
Db 301 CAACTGATGAGGTATTAAAGTTTGACACCATATCTGAGAAAACATCTGATCATTCAC 360
   |||

QY 457 TTCTTCCTTGGCCAACTGAACTGCCGACTCTATGAAAACCAAACTCTCCAGTTA 516
   |||
Db 361 TTCTTCCTTGGCCAACTGAACTGCCGACTCTATGAAAACCAAACTCTCCAGTTA 420
   |||

QY 517 GTATCAGCCCAATGCCCTTTTGGAGACAAATCCCTTAACCTTCAATGAGACTTCCAGAC 576
   |||
Db 421 GTATCAGCCCAATGCCCTTTTGGAGACAAATCCCTTAACCTTCAATGAGACTTCCAGAC 480
   |||

QY 577 ATGATGAGTGTGTATATGAGCCCAAGCTCCAGCCCTGACCTTCAAGAAAATGACAG 636
   |||
Db 481 ATGATGAGTGTGTATATGAGCCCAAGCTCCAGCCCTGACCTTCAAGAAAATGACAG 540
   |||

QY 637 CAATCCAGAGCGGCAATCAACAATGGGTGCCAATTAAGACCGAGCGCAATCACCGAT 696
   |||
Db 541 CAATCCAGAGCGGCAATCAACAATGGGTGCCAATTAAGACCGAGCGCAATCACCGAT 600
   |||

QY 697 GTCAATTCCTCGGAGGCAATCAATGAGCTCACTGTTCTGTGTGTTAAACCATTTAC 756
   |||
Db 601 GTCAATTCCTCGGAGGCAATCAATGAGCTCACTGTTCTGTGTGTTAAACCATTTAC 660
   |||

QY 757 TTCAAGGCGCTGTGGAAGTCAAAAGTTCAGCCCTGAGAACCAAGAAAGAACTGTTCTAC 816
   |||
Db 661 TTCAAGGCGCTGTGGAAGTCAAAAGTTCAGCCCTGAGAACCAAGAAAGAACTGTTCTAC 720
   |||

QY 817 AAGGCTGATGAGAGTGTGTGAGCACTATATGATGACAGGAAGCAAGTCCGCTTAT 876
   |||
Db 721 AAGGCTGATGAGAGTGTGTGAGCACTATATGATGACAGGAAGCAAGTCCGCTTAT 780
   |||

QY 877 CGGCGGCTGTGAGGACCAAGGTGCTTGAAGTGGCTTCAAGAGTGAATGACATCAC 936
   |||
Db 781 CGGCGGCTGTGAGGACCAAGGTGCTTGAAGTGGCTTCAAGAGTGAATGACATCAC 840
   |||

QY 937 ATGCTCTCATCTTGTCCCAAGCTGTGAGAAAGCTGTGCAAGGTGAGAAAGAACTCAC 996
   |||
Db 841 ATGCTCTCATCTTGTCCCAAGCTGTGAGAAAGCTGTGCAAGGTGAGAAAGAACTCAC 900
   |||

QY 997 CAGAGGTGTGAGAGTGTGTGAGTGAATGAGAGAGATGATGCTGTGTCCATG 1056
   |||
Db 901 CAGAGGTGTGAGAGTGTGTGAGTGAATGAGAGAGATGATGCTGTGTCCATG 960
   |||

QY 1057 CCGCGCTTCCGATTTGAGACGCGCTTCAATTGAGAGAGAGCTGCAAGACATGGGCTT 1116
   |||
Db 961 CCGCGCTTCCGATTTGAGACGCGCTTCAATTGAGAGAGAGCTGCAAGACATGGGCTT 1020
   |||

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QY 1117 GTGCATCTGTAGCCCTGAAAAGTCAAACCTCCAGGATATTGTGAGAAAGCCGAGAT 1176
   |||
Db 1021 GTGCATCTGTAGCCCTGAAAAGTCAAACCTCCAGGATATTGTGAGAAAGCCGAGAT 1080
   |||

QY 1177 GACCTCTAATGTCTCAGATGATTCATTAAGGCAATTTCTTGAAGTAAAGAAAGGCACT 1236
   |||
Db 1081 GACCTCTAATGTCTCAGATGATTCATTAAGGCAATTTCTTGAAGTAAAGAAAGGCACT 1140
   |||

QY 1237 GAAGAGCTGCAAGTACCGCTGTGTGATGTCTGCGCTTAAACCCCAACAGGGTG 1296
   |||
Db 1141 GAAGAGCTGCAAGTACCGCTGTGTGATGTCTGCGCTTAAACCCCAACAGGGTG 1200
   |||

QY 1297 ACTTTCAGGCGCAAGGCTTCTGCTTTTATAGAGAGTCTCTGAACCTATT 1356
   |||
Db 1201 ACTTTCAGGCGCAAGGCTTCTGCTTTTATAGAGAGTCTCTGAACCTATT 1260
   |||

QY 1357 ATCTTCATGGGCGAGAGTCCCAACCTTGTGTTAAGTAA 1395
   |||
Db 1261 ATCTTCATGGGCGAGAGTCCCAACCTTGTGTTAAGTAA 1299
   |||

RESULT 11
AAS83474
ID AAS83474 standard; cDNA; 2123 BP.
XX
AC AAS83474;
XX
DT 13-FEB-2002 (first entry)
XX
DE DNA encoding novel human diagnostic protein #19278.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW Food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX
OS Homo sapiens.
XX
PN MO200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US08631.
XX
PR 31-MAR-2000; 2000US-0540217.
PR 23-AUG-2000; 2000US-0649167.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Drmanac RT, Liu C, Tang YT;
XX
PT WPI; 2001-639362/73.
XX
PT F-PSDB; ABG19287.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity -
XX
PS Claim 1; SEQ ID No 19278; 103bp; English.
XX
CC The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations

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PT New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity
 XX
 PS Claim 1; SEQ ID No 19279; 103bp; English.
 XX
 CC The invention relates to isolated polynucleotide (I) and
 CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
 CC and gene mapping, and in recombinant production of (II). The
 CC polynucleotides are also used in diagnostics as expressed sequence tags
 CC for identifying expressed genes. (I) is useful in gene therapy techniques
 CC to restore normal activity of (II) or to treat disease states involving
 CC (II). (II) is useful for generating antibodies against it, detecting or
 CC quantitating a polypeptide in tissue, as molecular weight markers and as
 CC a food supplement. (II) and its binding partners are useful in medical
 CC imaging of sites expressing (II). (I) and (II) are useful for treating
 CC disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. AAs64197-AAs94564 represent novel human
 CC diagnostic coding sequences of the invention.
 CC Note: The sequence data for this patent did not appear in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 XX
 SO Sequence 1724 BP; 430 A; 439 C; 418 G; 437 T; 0 other;
 Query Match 36.7%; Score 512.4; DB 23; Length 1724;
 Best Local Similarity 79.9%; Pred. No. 9.2e-136;
 Matches 1195; Conservative 0; Mismatches 196; Indels 105; Gaps 46;

DB 675 TTAGTATACGCCAATGCGCTTTTGGAGACAATCCCTTACTTCATGAGACCTACGAG 734
 QY 573 GGACATCAGTAGGTTGTATATGAGCCCAAGCTCCAGCCC--TGACCTTCAAGAAA 629
 DB 735 GGACATCAGTAGGTTGTATATGAGCCCAAGCTCCAGCCCCTTGAGCTTCAAGGAAA 794
 QY 630 TGCAGAGCAAT--CCAGAGCGCCATCAACAAT--GGGTGTCATATAGCCGAAGGCG 686
 DB 795 TGCAGAGCAATTCAGAGCGCCCATCAACAATGGGGTGTCCATAAGACCGAAGGCG 854
 QY 687 AA--TCACCGATGTCATTCCTCGGAAG--CCATCAATAGCTCACTGTTCTG--GT 737
 DB 855 AATTACCGATGTTATTTCTCGGGAAGGCCATTTCAATAGCTCATGTTCTGGGTGG 914
 QY 738 GCTGTATACACCATTTACTTCAAGG--CCTGTGAAGTCAAAAGTTCAAGCCTGAGA 793
 DB 915 TGGGTTTAAACCATTTACTTCAAGGGCGCTGTGGAAGGTCAAAAGTTCAAGCCTGAGA 974
 QY 794 ACACAGAGGAAGAACTGTTTCAAGGCTGAT--GGAGAGTGTG--TTGAGATCTATG-- 849
 DB 975 ACACAGAGGAAGAACTGTTTCAAGGCTGATGGAGAGTGTGTTTCAAGATCTATGGA 1034
 QY 850 --ATGACCGAGGAAGCAAGTCCGTTAT--CGGCGCTGCTGAAGCAACCGAGTGT 906
 DB 1035 TGTTCACGAGGAAGCAAGTCCGTTATTCGGGCGCGCTGTGAAGCAACCGAGTGT 1094
 QY 907 --GAGTTCCTTCAAGAGTGATGATCA--CCATGTCCTCATCTTGGCCAGCC-- 959
 DB 1095 GATGTTGCTCCCTTCAAGAGTGATGATCA--CCATGTCCTCATCTTGGCCAGCCCTG 1154
 QY 960 TGAGAAAGACCTCGGCAAGTGAGAA--GGAATCAACCCAGAGGTGCT--GAGAGAG 1016
 DB 1155 AAGAAAGACCTCGGCAAGTGAGAAAGGAAGCACTACCCAGAGGTGCTTGCAGAGAG 1214
 QY 1017 GCTG--ATGAATTGAGAGATGATGCTGAGTGCATGATGCGCGCTT--CGGAT 1070
 DB 1215 GCTGGATGATTTTGAAGAGAGATGATGCTGATGCTGATGCTGATGCTGATGCTGAT 1274
 QY 1071 TGAGAGCGCTTCAAGTTGAAGAGACAGCTGCAAGACATGGGCTTGTGATCTGTTGAG 1130
 DB 1275 TGAGAGCGGCTTCAAGTTGAAGAGACAGCTGCAAGACATGGGCTTGTGATGAG 1334
 QY 1131 CCTGAAAGTCC-----AACTCCAGGATTTGTTGCAAGAG--CG 1172
 DB 1335 TCTTGTAGGCTCCCTGAAAGATCCCAAACTCCCGGATTTGTGCAAGAGGCGCG 1394
 QY 1173 AGATGACCTCTATGCTCAGATGCT--ATTCTAAGGCAATT--CTTGAAGTAATGA 1226
 DB 1395 AGATGACCTCTATGCTCAGATGCTCAGATGCTCAGATGCTCAGATGCTCAGATGCT 1454
 QY 1227 AGAAGGAGTGAAGCAG--CTGCAAGTA--CGCTGTGTTGATTTG--CTGACCGTTG--CTTA 1282
 DB 1455 AGAAGGAGTGAAGCAGCTGCAAGTACCGCTGTGTTGATTTGCTGACCGTTGCCCTAA 1514
 QY 1283 ACCCAAGAGGCTGAC--TTTCAAGGCAAGAGGCTTCTCT--GGTTTTTAAGAAGAG 1339
 DB 1515 ACCCAAGAGGCTGACCTTTCAAGGCAAGAGGCTTCTCTCTGAGTTTATTAAGAAGAG 1574
 QY 1340 TTCTCT--TGAACACTATTTATCTTCAATGGCAGAG--TAGCCAACTTGTGTTAA 1391
 DB 1575 TTCTCTTGAACACTATTTATCTTCAATGGGAGAGTTAGCCAACTTGTGTTAA 1630

RESULT 13
 ABA63081
 ID ABA63081 standard; DNA; 578 BP.
 XX
 AC ABA63081;
 XX
 DT 01-FEB-2002 (first entry)
 XX
 DE Human foetal liver single exon nucleic acid probe #11386.
 XX

Db 241 GTGCTGCAAGAGGCTGATGATGAGAGATATGCTGTGCTCCACATGCCCCG 300
 QY 1063 TTCCGATTCAGAGAGCGCTTCAGTTGAGAGACAGCTCAAGACATGGCCCTTGCGAT 1122
 Db 301 TTCCGATTCAGAGAGCGCTTCAGTTGAGAGACAGCTCAAGACATGGCCCTTGCGAT 360
 QY 1123 CTGTTCCAGCCCTGAAAAAGTCCAAACTCCCAAGTAT 1157
 Db 361 CTGTTCCAGCCCTGAAAAAGTCCAAACTCCCAAGTAT 395

RESULT 15

AAS83471
 ID AAS83471 standard; cDNA; 433 BP.

AC AAS83471;

DT 13-FEB-2002 (first entry)

DE DNA encoding novel human diagnostic protein #19275.

KW Human: chromosome mapping; gene mapping; gene therapy; forensic;
 food supplement; medical imaging; diagnostic; genetic disorder; ss.

XX Homo sapiens.

PN WO200175067-A2.

XX 11-OCT-2001.

PF 30-MAR-2001; 2001WO-US08631.

PR 31-MAR-2000; 2000US-0540217.

PR 23-AUG-2000; 2000US-0649167.

XX (HYSE-) HYSEQ INC.

PI Drmanac RT, Liu C, Tang YT;

DR WPI; 2001-639362/73.

DR P-PSDB; ABG19284.

PT New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity

PS Claim 1; SEQ ID No 19275; 103pp; English.

XX The invention relates to isolated polynucleotide (I) and
 CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
 CC and gene mapping, and in recombinant production of (II). The
 CC polynucleotides are also used in diagnostics as expressed sequence tags
 CC for identifying expressed genes. (I) is useful in gene therapy techniques
 CC to restore normal activity of (II) or to treat disease states involving
 CC (II). (II) is useful for generating antibodies against it, detecting or
 CC quantitating a polypeptide in tissue, as molecular weight markers and as
 CC a food supplement. (II) and its binding partners are useful in medical
 CC imaging of sites expressing (II). (I) and (II) are useful for treating
 CC disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. AAS64197-AAS94564 represent novel human
 CC diagnostic coding sequences of the invention.
 CC Note: The sequence data for this patent did not appear in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.

SO Sequence 433 BP; 113 A; 111 C; 108 G; 100 T; 1 other;

Query Match 24.4%; Score 340; DB 23; Length 433;
 Best Local Similarity 100.0%; Pred. No. 8.4e-87;
 Matches 340; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 623 AGGAAATGCAAGAGCAATCCAGAGCGGCATCAAAATGGGTGCAATAAGACCGAAG 682
 Db 93 AGGAAATGCAAGAGCAATCCAGAGCGGCATCAAAATGGGTGCAATAAGACCGAAG 152
 QY 683 GCCGATCACCGATGTCAATCCCTCGAAGAGCCATCATGAGCTCATCTGTGCTGG 742
 Db 153 GCCGATCACCGATGTCAATCCCTCGAAGAGCCATCATGAGCTCATCTGTGCTGG 212
 QY 743 TTAACACCATTTACTTCAAGGGCTGTGGAAGTCAAGCTTGAAGCAACAGGA 802
 Db 213 TTAACACCATTTACTTCAAGGGCTGTGGAAGTCAAGCTTGAAGCAACAGGA 272
 QY 803 AGGAATGCTTCTACAGGCTGATGAGAGTGTGTCAGCATCTATGATGTACAGGAAG 862
 Db 273 AGGAATGCTTCTACAGGCTGATGAGAGTGTGTCAGCATCTATGATGTACAGGAAG 332
 QY 863 GCAAGTCCGTTATCGGCGGTGCTGAAGGCAAGGAGTGTGAGTTGCTTCAAG 922
 Db 333 GCAAGTCCGTTATCGGCGGTGCTGAAGGCAAGGAGTGTGAGTTGCTTCAAG 392
 QY 923 GTGATGACATCACATGTGCTCTCATCTTGGCCCAAGCTGA 962
 Db 393 GTGATGACATCACATGTGCTCTCATCTTGGCCCAAGCTGA 432

Search completed: June 26, 2003, 22:33:45
 Job time : 356 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June '26, 2003, 22:13:10 ; Search time 214 Seconds
(without alignments)
1999.131 Million cell updates/sec

Title: US-09-828-592-6

Perfect score: 1395

Sequence: 1 atgtatccaatgtatagtag.....ccaacctgtgttaagtaa.1395

Scoring table: IDENTITY_NUC

Gapop 10.0, Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued_Patents_NA:*
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2: /cgn2_6/prodata/1/ina/5B.COMB.seq:*
3: /cgn2_6/prodata/1/ina/6A.COMB.seq:*
4: /cgn2_6/prodata/1/ina/6B.COMB.seq:*
5: /cgn2_6/prodata/1/ina/PCUS.COMB.seq:*
6: /cgn2_6/prodata/1/ina/Backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|--------|-------------|--------|----|-------------------|
| 1 | 1388.6 | 99.5 | 1395 | 1 | US-08-046-431A-1 |
| 2 | 1295.6 | 92.9 | 1382 | 3 | US-09-023-173-6 |
| 3 | 139.8 | 10.0 | 1194 | 4 | US-08-745-995A-28 |
| 4 | 139.8 | 10.0 | 1194 | 4 | US-08-745-995A-29 |
| 5 | 139.8 | 10.0 | 1492 | 4 | US-08-745-995A-25 |
| 6 | 139.8 | 10.0 | 1492 | 4 | US-08-745-995A-27 |
| 7 | 132 | 9.5 | 1179 | 4 | US-08-745-995A-22 |
| 8 | 132 | 9.5 | 1179 | 4 | US-08-745-995A-23 |
| 9 | 132 | 9.5 | 1414 | 4 | US-08-745-995A-19 |
| 10 | 132 | 9.5 | 1414 | 4 | US-08-745-995A-21 |
| 11 | 131 | 9.4 | 1393 | 1 | US-08-464-148-3 |
| 12 | 131 | 9.4 | 1393 | 1 | US-08-385-500-3 |
| 13 | 131 | 9.4 | 1393 | 1 | US-08-846-784-3 |
| 14 | 128.8 | 9.2 | 1197 | 4 | US-08-745-995A-10 |
| 15 | 128.8 | 9.2 | 1197 | 4 | US-08-745-995A-11 |
| 16 | 128.8 | 9.2 | 1358 | 4 | US-08-745-995A-7 |
| 17 | 128.8 | 9.2 | 1358 | 4 | US-08-745-995A-9 |
| 18 | 126.6 | 9.1 | 1191 | 4 | US-08-745-995A-34 |
| 19 | 126.6 | 9.1 | 1191 | 4 | US-08-745-995A-35 |
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| 21 | 126.6 | 9.1 | 1454 | 4 | US-08-745-995A-33 |
| 22 | 126.4 | 9.1 | 1191 | 4 | US-08-745-995A-4 |
| 23 | 126.4 | 9.1 | 1191 | 4 | US-08-745-995A-5 |
| 24 | 126.4 | 9.1 | 1584 | 4 | US-08-745-995A-1 |
| 25 | 126.4 | 9.1 | 1584 | 4 | US-08-745-995A-3 |
| 26 | 126.2 | 9.0 | 1260 | 4 | US-08-745-995A-16 |
| 27 | 126.2 | 9.0 | 1260 | 4 | US-08-745-995A-17 |

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| 28 | 126.2 | 9.0 | 1838 | 4 | US-08-745-995A-13 | Sequence 13, Appl |
| 29 | 126.2 | 9.0 | 1838 | 4 | US-08-745-995A-15 | Sequence 15, Appl |
| 30 | 124.6 | 8.9 | 1425 | 1 | US-08-464-148-1 | Sequence 1, Appl1 |
| 31 | 124.6 | 8.9 | 1425 | 1 | US-08-385-500-1 | Sequence 1, Appl1 |
| 32 | 124.6 | 8.9 | 1425 | 1 | US-08-846-784-1 | Sequence 1, Appl1 |
| 33 | 119 | 8.5 | 1152 | 1 | US-08-315-831A-13 | Sequence 13, Appl |
| 34 | 119 | 8.5 | 1152 | 1 | US-08-662-318-13 | Sequence 13, Appl |
| 35 | 119 | 8.5 | 1152 | 5 | PCT-US95-12509-13 | Sequence 13, Appl |
| 36 | 119 | 8.5 | 1316 | 1 | US-07-755-461A-12 | Sequence 12, Appl |
| 37 | 119 | 8.5 | 1316 | 1 | US-08-315-831A-12 | Sequence 12, Appl |
| 38 | 119 | 8.5 | 1316 | 1 | US-08-662-318-12 | Sequence 12, Appl |
| 39 | 119 | 8.5 | 1316 | 5 | PCT-US95-12509-12 | Sequence 12, Appl |
| 40 | 114 | 8.2 | 1365 | 3 | US-09-200-965-1 | Sequence 12, Appl |
| 41 | 112 | 8.0 | 1564 | 3 | US-08-948-997-1 | Sequence 1, Appl1 |
| 42 | 112 | 8.0 | 1564 | 4 | US-09-348-817A-1 | Sequence 1, Appl1 |
| 43 | 108.4 | 7.8 | 1950 | 2 | US-08-472-659-30 | Sequence 30, Appl1 |
| 44 | 108.4 | 7.8 | 1950 | 2 | US-08-474-661-30 | Sequence 30, Appl1 |
| 45 | 108.4 | 7.8 | 1950 | 2 | US-08-611-977-30 | Sequence 30, Appl1 |

ALIGNMENTS

RESULT 1
US-08-046-431A-1
Sequence 1, Application US/08046431A
Patent No. 5420252
GENERAL INFORMATION:
APPLICANT: KATO, HIROYUKI
APPLICANT: YOSHITAKE, SHINJI
APPLICANT: SUZUKI, SUGURA
APPLICANT: SUZUKI, NOBORU
APPLICANT: SETO, TOSHIO
APPLICANT: NAKAO, NAOKO
APPLICANT: MIZUI, YOSHITARU
TITLE OF INVENTION: HUMAN ANTITHROMBIN III MUTANT
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: FLYNN, THEIL, BOUTELL & TANIS, P. C.
STREET: 2026 Rambling Road
CITY: Kalamazoo
STATE: Michigan
COUNTRY: USA
ZIP: 49008-1699
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inches, 1.44 Mb storage
COMPUTER: IBM PC/XT/AT Compatible
OPERATING SYSTEM: MS-DOS 5.0
SOFTWARE: WordPerfect 5.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/046,431A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP90488
FILING DATE: 10-APR-1992
APPLICATION NUMBER: JP1855
FILING DATE: 22-FEB-1993
ATTORNEY/AGENT INFORMATION:
NAME: Terryence F. Chapman
REGISTRATION NUMBER: 32549
REFERENCE/DOCKET NUMBER: Puriya Case 1286
TELECOMMUNICATION INFORMATION:
TELEPHONE: (616) 381-1156
TELEFAX: (616) 381-5465
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1395 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORIGINAL SOURCE:

ORGANISM: Homosapien
 FEATURE: CDS
 NAME/KEY: 1..1395
 LOCATION: sig_peptide
 NAME/KEY: 1..96
 LOCATION: mat_peptide
 NAME/KEY: 97..1395
 LOCATION: 97..1395

US-08-046-431A-1

Query Match 99.5%; Score 1388.6; DB 1; Length 1395;
 Best Local Similarity 99.7%; Pred. No. 0;
 Matches 1391; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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 DB 61 TTGCTGCTCATTTGGCTTCTGGAAGCTGTAACCTCTGTAAGAGCCCTGTGACATCTGC 120
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 DB 121 AAGAGCAAGCCGCGGAGCATTTCCATGATGCCATGTTTACCGCTCCCGGAGAG 180
 QY 181 AAGGCAACTGAGAGTGAAGGCTGAGAAAGAGATCCCGAGGCGCAACCGGCGTGC 240
 DB 181 AAGGCAACTGAGAGTGAAGGCTGAGAAAGAGATCCCGAGGCGCAACCGGCGTGC 240
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 DB 241 TGGGAACCTGTCGAAGCCCAATTCGCGCTTGTCTACCACTTTCTATCAGCACTGCGAGAT 300
 QY 301 TCCAAAGATGACATATATATATTTCTGTCACCCCTGAGTATCTCCAGGCTTTTGTCT 360
 DB 301 TCCAAAGATGACATATATATATTTCTGTCACCCCTGAGTATCTCCAGGCTTTTGTCT 360
 QY 361 ATGACCAAGCTGAGGCTGCTGTATGACACCCCTCAGCACTGATGAGGATTTAAGTTT 420
 DB 361 ATGACCAAGCTGAGGCTGCTGTATGACACCCCTCAGCACTGATGAGGATTTAAGTTT 420
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 DB 541 GACCAATCCCTTACCTTCAATGAGACCTTACAGAGCATCAGTATGATGAGAGCC 600
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 QY 661 TGGGTGTCATTAAGACCGAAGCCGATATCCGATGTCATCTCCCTGGAAGCATCAAT 720
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 QY 721 GAGCTCACTGTTCTGCTGCTGTTAACACCAATTTACTTCAAGGCGCTGTGAAGTCAAG 780
 DB 721 GAGCTCACTGTTCTGCTGCTGTTAACACCAATTTACTTCAAGGCGCTGTGAAGTCAAG 780
 QY 781 TTGAGCCCTGAGAACACAAAGAAAGAACTGTTTCAAGGCTATGAGAGTGTGTTCA 840
 DB 781 TTGAGCCCTGAGAACACAAAGAAAGAACTGTTTCAAGGCTATGAGAGTGTGTTCA 840
 QY 841 GCATCTATGATGTACAGAAAGCAAGTTCGTTATCGGCGCGTGTGAAGGCAACCCAG 900
 DB 841 GCATCTATGATGTACAGAAAGCAAGTTCGTTATCGGCGCGTGTGAAGGCAACCCAG 900

QY 901 GTGCTTGAGTTCGCCCTTCAAGAGTATGATGATCACTGATGCTCATCTTCCCAAGCCT 960
 DB 901 GTGCTTGAGTTCGCCCTTCAAGAGTATGATGATCACTGATGCTCATCTTCCCAAGCCT 960
 QY 961 GAGAAAGCCTGCGCAAGAGTGAAGAAAGAACTCAACCCAGAGGCTGAGAGAGTGGCTG 1020
 DB 961 GAGAAAGCCTGCGCAAGAGTGAAGAAAGAACTCAACCCAGAGAGTGGCTGAGAGAGTGGCTG 1020
 QY 1021 GATGATGAGAGAGATGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTG 1080
 DB 1021 GATGATGAGAGAGATGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTG 1080
 QY 1081 TTCACTTGAAGAGAGAGCTGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1140
 DB 1081 TTCACTTGAAGAGAGAGCTGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1140
 QY 1141 TCCAAACTCCAGAGATGTTGTCAGAAAGCCGAGAGAGAGAGAGAGAGAGAGAGAGAG 1200
 DB 1141 TCCAAACTCCAGAGATGTTGTCAGAAAGCCGAGAGAGAGAGAGAGAGAGAGAGAGAG 1200
 QY 1201 CATAAGCATTTCTTGAAGTAAATGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1260
 DB 1201 CATAAGCATTTCTTGAAGTAAATGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1260
 QY 1261 GTGATGCTGAGCCGCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1320
 DB 1261 GTGATGCTGAGCCGCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1320
 QY 1321 CTGCTTTTATGAAGAGAGTCTCTGAGACCTATTTATCTTCAAGGAGAGAGAGAGAG 1380
 DB 1321 CTGCTTTTATGAAGAGAGTCTCTGAGACCTATTTATCTTCAAGGAGAGAGAGAGAG 1380
 QY 1381 CTTGTGTTAAGTAA 1395
 DB 1381 CTTGTGTTAAGTAA 1395

RESULT 2
 US-09-023-173-6
 ; Sequence 6, Application US/09023173
 ; Patent No. 6066781
 ; GENERAL INFORMATION:
 ; APPLICANT: Sutcliffe, Thomas D.
 ; APPLICANT: Rodriguez, Raymond L.
 ; TITLE OF INVENTION: Production of Mature Proteins
 ; TITLE OF INVENTION: in Plants
 ; NUMBER OF SEQUENCES: 23
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Dehlinger & Associates
 ; STREET: 350 Cambridge Ave., Suite 250
 ; CITY: Palo Alto
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94306
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FASTSEQ for Windows Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/023,173
 ; FILING DATE: 13-FEB-1998
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION NUMBER: 60/038,168
 ; FILING DATE: 13-FEB-1997
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Petichory, Joanne R
 ; REGISTRATION NUMBER: P42995
 ; REFERENCE/DOCKET NUMBER: 0665-0007.30
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 650-324-0880

TELEFAX: 650-324-0960
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1382 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 IMMEDIATE SOURCE:
 CLONE: codon opt Ramy3D-native mature ATIII
 US-09-023-173-6

Query Match 92.9%; Score 1295.6; DB 3; Length 1382;
 Best Local Similarity 98.9%; Pred. No. 0;
 Matches 1304; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

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QY 198 GGGCTCAGAAAGAGATCCGAGGCGCCACCAACCGGCGTGTCTGAGAACTGTCCAAAGG 257
DB 177 GGGCTCAGAAAGAGATCCGAGGCGCCACCAACCGGCGTGTCTGAGAACTGTCCAAAGG 236
QY 258 CAATTCCTGCTTGTCTACCACTTTCTATAGACACCTGAGAGATTCGAAGATGACATTA 317
DB 237 CAATTCCTGCTTGTCTACCACTTTCTATAGACACCTGAGAGATTCGAAGATGACATTA 296
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DB 297 TAAACATTTCTGTACACCCCTGAGATATCCACGCGCTTGTGATAGCAACACTGGGATGC 356
QY 378 CTGTAATGACACCCCTCCAGCAACTGATGAGGATTTAAATTGAACCATATCTGAGAA 437
DB 357 CTGTAATGACACCCCTCCAGCAACTGATGAGGATTTAAATTGAACCATATCTGAGAA 416
QY 438 AACATCTGATGATGATCACTCTTCTTTGCCAACTGAATCTGCCGACTTATGCAAAAGC 497
DB 417 AACATCTGATGATGATCACTCTTCTTTGCCAACTGAATCTGCCGACTTATGCAAAAGC 476
QY 498 CAACAATCTCTCAAGTTAGTATCAGCCCAATGCGCTTTTGGAGCAAAATCCCTTAACCT 557
DB 477 CAACAATCTCTCAAGTTAGTATCAGCCCAATGCGCTTTTGGAGCAAAATCCCTTAACCT 536
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DB 537 CAATGAGACTTACCAAGACATGATGATGATGATGAGGCAAGCTCCAGCCCTGGA 596
QY 618 CTTCAGAGAAATGACAGACATCCAGAGCGGCATCAAAATAGGTGTCCATTAAGAC 677
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QY 678 CGAAGCGCGAATCACCGATGATTCCTCCGGAAGGCATCAATGAGCTCACTGTTCTGGT 737
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QY 738 GCTGTTAACACCATTTACTTCAAGGCGCTGTGAGAGTCAAAATTCAAGCCCTGAGAACAC 797
DB 717 GCTGTTAACACCATTTACTTCAAGGCGCTGTGAGAGTCAAAATTCAAGCCCTGAGAACAC 776
QY 798 AAGGAAGAACTGTTCTTACAGGCTGATGAGAGTGTGTCTACGATCTATATATGATCA 857
DB 777 AAGGAAGAACTGTTCTTACAGGCTGATGAGAGTGTGTCTACGATCTATATATGATCA 836
QY 858 GGAAGGCAAGTTCCTGTTATCGCGCGTGTGAGAGCAACCAAGTGTGAGTGTGAGTCCCT 917
DB 837 GGAAGGCAAGTTCCTGTTATCGCGCGTGTGAGAGCAACCAAGTGTGAGTGTGAGTCCCT 896
QY 918 CAAGGTGATGATCATCAACATGCTCTCATCTTGGCCCAAGCCTGAGAAAGCCTGAGCA 977

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DB 897 CAAGGTGATGATCATCAACATGATGCTCATCTTGTGCCAAGCCTGAGAAAGCCTGAGCA 956
QY 978 GGTGAGAAAGAACTCACCCCGAGAGTCTCTCAGAGAGTGTGATGAAATTGAGAGAT 1037
DB 957 GGTGAGAAAGAACTCACCCCGAGAGTCTCTCAGAGAGTGTGATGAAATTGAGAGAT 1016
QY 1038 GATGCTGTGTGTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1097
DB 1017 GATGCTGTGTGTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1076
QY 1098 GCTGCAAGACATGAGCGCTTGTGATGATGATGATGATGATGATGATGATGATGATGAT 1157
DB 1077 GCTGCAAGACATGAGCGCTTGTGATGATGATGATGATGATGATGATGATGATGATGAT 1136
QY 1158 TGTTCGCAAGAGCGCGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1217
DB 1137 TGTTCGCAAGAGCGCGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1196
QY 1218 GGTAAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1277
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DB 1257 GCTAAACCCCAACAGGCTGATCTTCAAGGCGCAACAGGCTTCTGCTTTTATTAAGAG 1316
QY 1338 AGTTCCTGTAACATATATCTTCAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1395
DB 1317 AGTTCCTGTAACATATATCTTCAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1374

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RESULT 3 US-08-745-995A-28

Sequence 28, Application US/08745995A

Patent No. 6372887

GENERAL INFORMATION:

APPLICANT: Silver, Gary M.

APPLICANT: Wisniewski, Nancy

TITLE OF INVENTION: No. 6372887a) Serine Protease Inhibitor

TITLE OF INVENTION: Nucleic Acid Molecules, Proteins

NUMBER OF SEQUENCES: 41

CORRESPONDENCE ADDRESS:

ADDRESSEE: Heekel Corporation

STREET: 1825 Sharp Point Drive

CITY: Fort Collins

STATE: Colorado

COUNTRY: USA

ZIP: 80525

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: Windows 95

SOFTWARE: WordPerfect for Windows, Version 7.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/745,995A

FILING DATE: 07-NOV-1996

CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:

NAME: Verrier, Carol Talkington

REGISTRATION NUMBER: 37,459

REFERENCE/DOCKET NUMBER: PC-2

TELECOMMUNICATION INFORMATION:

TELEPHONE: 970/493-7272

TELEFAX: 970/484-9505

INFORMATION FOR SEQ ID NO: 28:

SEQUENCE CHARACTERISTICS:

LENGTH: 1194 nucleotides

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

US-08-745-995A-28

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| Query Match | 10.0%; | Score 139.8; | DB 4; | Length 1194; |
| Best Local Similarity | 49.5%; | Pred. No. 2.1e-29; | | |
| Matches 419; | Conservative | 0; | Mismatches 422; | Indels 6; |
| | | | | Gaps 2 |

| | | | |
|----|------|--|------|
| QY | 489 | TCGAAAAGCCCAACAATCTCCCAAGTTAGTATCGAGCCAAATGGCCCTTTTGTGAGACAAATTC | 548 |
| Db | 297 | TCTTAATATCACAAAAAGGTGTAACTCTGGAAATTGCCAATAAAGTTTATGTATTGAAAGG | 356 |
| QY | 549 | CCTTAACCTTCAATGAGACTTACAGAGACATCAGTGAAGTTGGTATATGAGGCCAACTCCA | 608 |
| Db | 357 | CTAATACATTTAAACCCACCTTTCMAAGAGTTGCCACCAACAAATCTTAGCTGAGACAGA | 416 |
| QY | 609 | GCCCTGGACTTCAAGAAAATGACAGACCAATCCAGAGCGGCCATCAACAAATGGGTGTC | 668 |
| Db | 417 | AAACTGAACTTTGCCCCAAAATGCTGAAAGCCCTAAA---GTTATCAACACTTGGGTGGA | 473 |
| QY | 669 | CAATPAGACCGAAGCCGAATCACCGATGTCATTCCTCGAAGCCATCAATGACTCAC | 728 |
| Db | 474 | AGAAAAAACTCATGCACAAATTCATGATTTGATCAAAACCGGTGATCTGACACAGAAATTC | 533 |
| QY | 729 | TGTTCTGGTGTGGTTAACACATTTACTTCAAGGCGCTGTGGAAGTCAAAAGTTCAAGCC | 788 |
| Db | 534 | AAGAAATGTTCTTGCAATGCAATGTACTTCAAGGCTCTTGGGAAAAACAATTCAGAA | 593 |
| QY | 789 | TGAGAACACAAGAAAGAACTGTTCTACAAAGCTAGTGAAGAGTGTGTGACATCTAT | 848 |
| Db | 594 | GGAAAAACCCAAAGCAAAACCTTTCTATGTTACTGAAAACAGGACAAAGAAATGTACGAA | 653 |
| QY | 849 | GATGTACCAAGAGGCAAGTTCCGTTATTCGGCGGTGGCTGA--AGGCATCCCAAGTGTCT | 905 |
| Db | 654 | GATGCACATTTAAGATTAATTCGGTTATGAGAAATTTAAGAAATTAAGATTCGCAAGGCTGT | 713 |
| QY | 906 | TGAGTTGGCCCTTCAAAAGGTGATGACATCAACATGGTCCATCTTGGCCCAAGCTGAGAA | 965 |
| Db | 714 | AGAATTTGCCCTTACAGGAACTCAGATTTTGGCATGTTAATCATTTTGGCCAAACAGCAAAAC | 773 |
| QY | 966 | GAGCTTGCCCAAGTGAAGAAAGAACTCAACCCAGAGGTGCTGAGAGTGGCTGATGA | 1025 |
| Db | 774 | TGTCCTCCCCACTCTTGAAGAAAAAATTCACAAATGTTGATTTGGCAAACTTGACTCAACG | 833 |
| QY | 1026 | ATTGAGAGAGATGATGCTGTGTGCTCCACATGCGCCGCTTCGSCATTTGAGAGCGCTTACG | 1085 |
| Db | 834 | CATGACTCTGTTGAAGTTATTTTGGATCTGCTAAATTCAAATATGAGTCTGAAATTTA | 893 |
| QY | 1086 | TTTGAAGAGAGAGCTGCAAGACATGGGCTTGTGCATCTGTTCAAGCCCTGAAAAGTCCAA | 1145 |
| Db | 894 | TTTGAAATGATCCTCTGAAAAAAGTTGGATATGTCGATATGTTTCATGCGCTGGAAAAAGCTGA | 953 |
| QY | 1146 | ACTCCCAAGTATTTGTCAGAAAGCCGAGATGACCTCTATGTCCTAGATGATTCATATA | 1205 |
| Db | 954 | TTTCAAAAGATGCTTGAAGGATCTGATGAGATGTTATATATTTTAAAGTAAATTCAAA | 1013 |
| QY | 1206 | GGCATTTCCTTAGAGTAATGAAAGAGCAGTGAACAGCTGCATACCGCTGTGTGAT | 1265 |
| Db | 1014 | AGCTTTCAATTTGAAGTAATGAAAGAGGTGCTGAACCTGCAGCTGCCACAGGGGTGATGTT | 1073 |
| QY | 1266 | TGCTGGCCGTTGCTTAAACCCCAACAGGGTGACTTTCAAGGCCAACAGGCTTTTCTGGT | 1325 |
| Db | 1074 | AATGATGCGTTGTATGCCAATGATGCCAATGGCCTTCAATGCTGAGACATTCATCTCTGA | 1133 |
| QY | 1326 | TTTTATA 1332 | |
| Db | 1134 | CTTCTTA 1140 | |

RESULT 4
 US-08-745-995A-29/c
 ; Sequence 29, Application US/08745995A
 ; Patent No. 6372887
 ; GENERAL INFORMATION:
 ; APPLICANT: Silver, Gary M.
 ; APPLICANT: Wisniewski, Nancy

TITLE OF INVENTION: No. 6372887e1 Serine Protease Inhibitor
 TITLE OF INVENTION: Nucleic Acid Molecules, Proteins
 TITLE OF INVENTION: and Uses Thereof
 NUMBER OF SEQUENCES: 41
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Heska Corporation
 STREET: 1825 Sharp Point Drive
 CITY: Fort Collins
 STATE: Colorado
 COUNTRY: USA
 ZIP: 80525
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: Windows 95
 SOFTWARE: Wordperfect for Windows, Version 7.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/
 FILING DATE: 07-NOV-1996
 CLASSIFICATION: 536
 ATTORNEY/AGENT INFORMATION:
 NAME: Verser, Carol Talkington
 REGISTRATION NUMBER: 37,459
 REFERENCE/DOCKET NUMBER: FC-2
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 970/493-7272
 TELEFAX: 970/484-9505
 INFORMATION FOR SEQ ID NO: 29:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1194 nucleotides
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: CDNA

| | Query Match | 10.0% | Score 139.8 | DB 4 | Length 1194 |
|----|---|----------------|-------------------|----------|-------------|
| | Best Local Similarity | 49.5% | Pred. No. 2.1e-29 | | |
| | Matches 415 | Conservative 0 | Mismatches 422 | Indels 6 | Gaps 2 |
| Qy | 489 TCGAAGAGCCACCAATCTCCAGTTAGTATGACGCCAATCGCCCTTTTGGAGACAATC | | | | 548 |
| Db | 898 TCTTAATATACCAAAAAGSTGTACTGTGAATATGCCAATTAAGTTATGTTATGAAAG | | | | 839 |
| Qy | 549 CCTTACCTTCAATGAGCTTACAGGACATCAGTAGTGGTATATGAGGCAAGCTCCA | | | | 608 |
| Db | 838 CTATACATTTAAAACCCACTTCGAAAGAGTGGCCACCAACAAATCTTAGCTGAGACGA | | | | 779 |
| Qy | 609 GCCCTGGACTTCAAGAAATGACGAGCAATCCAGAGCGGCGCATCAACAATGGGTGTC | | | | 668 |
| Db | 778 AACTTTAATCTTGCCCAAAATGCTGAAGGCGCTAA---GTATCAACCTTGGGTGGA | | | | 722 |
| Qy | 669 CATTAAAGACGAGGCGGAATCAACCGATGTCTATTCCTCGGAAGCCATCAATGAGCTAC | | | | 728 |
| Db | 721 AGAAAAAATCATACAAAATTTATATGATTTGATCAAAAGCGGTGATCTAGACGAGATTC | | | | 662 |
| Qy | 729 TGTTCGTGCTGTTAAACACATTTACTTCAAGGCGCTGTGCAATCAAGTTCAAGCC | | | | 788 |
| Db | 661 AAGATGTTCTTGTCAATGATGTACTTTCAGAGGCTTTGGAGAAACAATTCAGAA | | | | 602 |
| Qy | 789 TGAACAACAAGAGAGAACTGTTCACAAAGCGTATGAGAGTGGTTCAGCATCAT | | | | 848 |
| Db | 601 GGAATAACACCCAAACAAACCTTCTATGTATTCTGAAACAGAGACAAGATGTACCAAT | | | | 542 |
| Qy | 849 GATGTACAGAAAGCAAGTTCGTTATCGCGCGGTGGCTGA---AGGCAACCGAGTGT | | | | 905 |
| Db | 541 GATCAACAATTAAAGATTAATTCGTTATGAGAAATTTGAAGAAATTAGATGCGAAGCGT | | | | 482 |
| Qy | 906 TGAAGTCCCTTCAAGAGTATGACATCAACCATGTCCTCATCTTGGCCCAAGCCTGAGA | | | | 965 |
| Db | 481 AGATTTGCCCTACGAAATCAAGTTGGGCATGTATATCATTTTGGCAACAGCAAAAC | | | | 422 |
| Qy | 966 GAGCCTGCGCAAGGTGAGAAAGAACTACCCCAAGAGTGTGACGAGATGGCTGATGTA | | | | 1025 |

```

Db      421 TGGTCTCCCACTCTTGGAAGAAAATTACAAAATTGATTTGGCAAACTTGACTCAACG 362
Qy      1026 ATTGAGGAGATGATGCTGTGTGTCACATGCCCCGCTTCGCGATTGAGAGCGGCTTCAG 1085
Db      361 CATGTAACCTGTGTGAAGTTATTTTGGATCTGCTTAATTAATAATTGAGTCTGAATTTAA 302
Qy      1086 TTGGAAGAGCAGCTGCAAGACATGGGCTTGTGATCTGTTCAGCCCTGAAAGTCCAA 1145
Db      301 TTTGATATATCTCTGGAAGAAAGTTGGATATGTCTATATGTTCAAGCTTGAGAAAGCTGA 242
Qy      1146 ACTCCAGGATATGTTGGAGAGGCGGAGATGACCTATGTCAGATGCAATTCATTA 1205
Db      241 TTTCAAGAGATTCCTTGAGAGATCTGATGAGATGTTATTTCTTAAGTAATTCAAA 182
Qy      1206 GGCAATTTCTTGAGTAATGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1265
Db      181 AGCTTTCAATGAATGAATGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 122
Qy      1266 TGCTGCGGCTTGCCTAAACCCCAAGGAGTCTTCAAGGCAACAGGCTTTCCTGT 1325
Db      121 AATGATGGGTGTATGCAATGATGCAATGAGCTTCAATGCTGAGCAATCCATTCCTTA 62
Qy      1326 TTTTATA 1332
Db      61 CTTCTTA 55

```

RESULT 5

US-08-745-995A-25
Sequence 25, Application US/08745995A

GENERAL INFORMATION:

APPLICANT: Silver, Gary M.
APPLICANT: Wisniewski, Nancy
TITLE OF INVENTION: No. 6372887el Serine Protease Inhibitor
TITLE OF INVENTION: Nucleic Acid Molecules, Proteins
TITLE OF INVENTION: and Uses Thereof
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:

ADDRESSEE: Heeka Corporation
STREET: 1825 Sharp Point Drive
CITY: Fort Collins
STATE: Colorado
COUNTRY: USA

ZIP: 80525

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: WordPerfect for Windows, Version 7.0
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/745,995A
FILING DATE: 07-NOV-1996

CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:

NAME: Verber, Carol Talkington
REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: PC-2
TELECOMMUNICATION INFORMATION:

TELEPHONE: 970/493-7272
TELEFAX: 970/464-9505

INFORMATION FOR SEQ ID NO: 25:

SEQUENCE CHARACTERISTICS:

LENGTH: 1492 nucleotides

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

FEATURE:

NAME/KEY: CDS

LOCATION: 3..1196

US-08-745-995A-25

Query Match 10.0%; Score 139.8; DB 4; Length 1492;
Best Local Similarity 49.5%; Seed No. 2.3e-29;
Matches 419; Conservative 0; Mismatches 422; Indels 6; Gaps 2;

```

Qy      489 TCGAAAAGCCCAAAATCTCTCAAGTATGATGAGCCATCGCCTTTTGGAGACAATC 548
Db      299 TCTTATATACAAAAGGTGTATCTGTGAATATGCGAATTAAGTTATATGTAAGG 358
Qy      549 CTTTACCTTCAATGAGACCTTACAGAGACATGAGTGTATATGAGACCAAGTCCA 608
Db      359 CTATACCTTAAACCCACCTTCAAGAGTGGCAACCAAAATCTTACCTGAGAGAGA 418
Qy      609 GCCCTGAGCTTCAAGAAAATGACAGCAATCCAGAGCGGACCATCAACAAATGGGTGC 668
Db      419 AATCTTAACTTTGCCAAAATGTGAAAGCGTAA--CTTATCAACTTTGGTTGA 475
Qy      669 CAATAGACCGAAGCGCAATCAACGATGATTCCTCGGAAGCCATCAATAGCTCAC 728
Db      476 AGAAAAAATCATGACAAAATTCATGATTTGATCAAGCCGATCTAGACGAGATTC 535
Qy      729 TGTCTGTGTGTGTTAAACATTTACTTCAAGGCGCTGTGAACTCAAGTCAAGCCC 788
Db      536 AAGATGTTCTTGTCAATGATGATTTCAAGGCTTTTGGAGAAACATTCAGAA 595
Qy      789 TGAGACACAAGAAAGGAACTGTTCTCAAGGCTGATGAGAGTCTGTTCAGATCTAT 848
Db      596 GAAAACACCCAGACAAACCTTTCTATGTTACTGAAACAGACAAAGATGACGAT 655
Qy      849 GATGTACAGAGAAAGCAATTCCTGTTATCGGCGGCTGAGTAA--AGGACCCAGGTCT 905
Db      656 GATGACATTTAAGATTAATTCCTTATGAGAAATTTGAAGATTAATGATGCAAGGCTGT 715
Qy      906 TGAATGCGCTTCAAGATGATGATCAATCAATGATGATCTTGGCCAAAGCTGAGAA 965
Db      716 AGAATGCGCTTCAAGAACTGATGATTTGGCCATTTATATCTTTTGGCAACAGCAAAAC 775
Qy      966 GAGCGTGGCAAGGTGAGAGAACTCACCCAGAGGTGCTGAGAGAGTGTGATGA 1025
Db      776 TGTCTCCCACTCTTGAGAGAAATTAACAAATGTTGATTTGCAAAACTTGACATCAAG 835
Qy      1026 ATTGAGGAGATGATGCTGTGTGTCACATGCCCCGCTTCGCGATTGAGAGCGGCTTCAG 1085
Db      836 CATGTAACCTGTGAAGTTATTTTGGATCTGCTTAAATTCAAAATGAGTCTGAATTTAA 895
Qy      1086 TTGGAAGAGCAGCTGCAAGACATGGGCTTGTGATCTGTTCAGCCCTGAAAGTCCA 1145
Db      896 TTTGATATATCTCTGGAAGAAAGTTGGATGTCTGATATGTTCAATGCTGGAAGAGCTGA 955
Qy      1146 ACTCCAGGATATGTTGGAGAGGCGGAGATGACCTATGTCAGATGCAATTCATTA 1205
Db      956 TTTCAAGAGATTCCTTGAGAGATCTGATGAGATGTTATTTCTTAAGTAATTCAAA 1015
Qy      1206 GGCAATTTCTTGAGTAATGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1265
Db      1016 AGCTTTCAATGAATGAATGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1075
Qy      1266 TGCTGCGGCTTGCCTAAACCCCAAGGAGTCTTCAAGGCAACAGGCTTTCCTGT 1325
Db      1076 AATGATGGGTGTATGCAATGATGCAATGAGCTTCAATGCTGAGCAATCCATTCCTTA 1135
Qy      1326 TTTTATA 1332
Db      1136 CTTCTTA 1142

```

RESULT 6

US-08-745-995A-27/c

Sequence 27, Application US/08745995A

Patent No. 6372887

GENERAL INFORMATION:

APPLICANT: Silver, Gary M.
APPLICANT: Wisniewski, Nancy

TITLE OF INVENTION: No. 637287el Serine Protease Inhibitor
 TITLE OF INVENTION: Nucleic Acid Molecules, Proteins
 NUMBER OF INVENTION: and Uses Thereof
 NUMBER OF SEQUENCES: 41
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Heska Corporation
 STREET: 1825 Sharp Point Drive
 CITY: Fort Collins
 STATE: Colorado
 COUNTRY: USA
 ZIP: 80525
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: Windows 95
 SOFTWARE: Wordperfect for Windows, Version 7.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/745,995A
 FILING DATE: 07-NOV-1996
 CLASSIFICATION: 536
 ATTORNEY/AGENT INFORMATION:
 NAME: Verser, Carol Talkington
 REGISTRATION NUMBER: 37,459
 REFERENCE/DOCKET NUMBER: FC-2
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 970/493-7272
 TELEFAX: 970/484-9505
 INFORMATION FOR SEQ ID NO: 27:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1492 nucleotides
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 US-08-745-995A-27

Query Match 10.0%; Score 139.8; DB 4; Length 1492;

Best Local Similarity 49.5%; Pred. No. 2.3e-29; Matches 419; Conservative 0; Mismatches 422; Indels 6; Gaps 2;

QY 489 TCGAAGAGCCCAAAATCTCCCAAGTAGATCAGCCCAATGCTTTTGGAGACAATC 548
 DB 1194 TCTTAATACCAAAAAGTGAATCTGGAATTTGCCAATTAAGTTATGTATGAGAG 1135
 QY 549 CTTACCTTCATGAGACCTTACAGACATCAGTGAATGATATGAGCCCAAGCTTCA 608
 DB 1134 CTATACATTAACCAACCTTCAAGAGAGTTGCCACCAAAATTTTACCTGAGACAG 1075
 QY 609 GCCCTGAGCTTCAAGAAAATGCAAGCAATCCAGAGCGGCATCAACAAATGGGTGC 668
 DB 1074 AAACCTGAACCTTGGCCCAAAATGCTGAAGCGCTAA--GTTATCAACCTTGGGTGA 1018
 QY 669 CATAAGACCGAAGCGCAATCCAGATGCTATTCCTCGGAAGCATCAATGAGCTCAG 728
 DB 1017 AGAAAAACCTCAGACAAATTCATGATTCATCAAAAGCGGATCTAGACAGATTC 958
 QY 729 TGTTCGTGCTGTTTACCACTTACTTCAAGGCTGTGAAGTCAAGTTCAGGCC 788
 DB 957 AAGAAATGTTCTTGTCAATCATTTGATCTTCAAGGCTTGGAGAAACAATTCAGAA 898
 QY 789 TGAAGACACAGAGAGAACTGTTCTACAGAGCTGAAGAGTCCGTTCCACATCTAT 848
 DB 897 GGAAGAACCCCAAGACAACTTCTTCTATGTTACTGAAACAGAGACAAAGATTTACGAT 838
 QY 849 GATGTACCAAGAGAGCAAGTTCCTTATCGGCGCTGCTGA--AGGCAACCGAGTGT 905
 DB 837 GATGCAATTAAGATTAATTCGTTATGAGAAATTTGAAGATTAATGATGCCAAGGTGT 778
 QY 906 TGAATGCTCTTCAAGAGTATGACATCACTGATGCTTCTCATTTGCCCAAGCTTGA 965
 DB 777 AGAATGCTCTTCAAGAGTATGACATCACTGATGCTTCTCATTTGCCCAAGCTTGA 718
 QY 966 GACCTGCGCAAGTGAAGAGAACTCACCACAGAGTCTCTGAGAGTGGCTGATGA 1025

DB 717 TGGTCTCCCACTCTTGAAGAAAATTTACAAATTTGATTTGCAAACTTACTCAGC 658
 QY 1026 ATTGAGAGATGATGCTGTGTGTCCACATGCCCCGCTCCGATTTGAGAGCGCTTCA 1085
 DB 657 CATGTAATCTGTGAAGTATTTTGGATCTGCTTAAATTTGAATTTGATTTGAATTTA 598
 QY 1086 TTTGAAGAGACGCTGCAAGACATGAGGCTTGTGATCTGTTGACGCTGAAAAGTCCA 1145
 DB 597 TTTGAATGATCTCTGAAAAGAGTGTGATGCTGATATGTTCAAGCTCGAAAAGCTGA 538
 QY 1146 ACTCCAGGATTTGTCAGAGAGCGCAGATGACCTCATGCTCAGATGATTCATTA 1205
 DB 537 TTTCAAGGATTTGTTGAAGAGATCTGATGAGATTTATTTTAAAGTATTTCAAA 478
 QY 1206 GGCATTTCTTGAAGTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1265
 DB 477 AGCTTTCAATTAAGTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 418
 QY 1266 TGGTGGCTTGTGCTTAAACCCCAAGAGGTGACTTTCAAGGCTCAACAGGCTTTCTGT 1325
 DB 417 AATGATGCTGTATGCAATGATGCAATGCTTCAATGCTGAGATTCATTCCTGA 358
 QY 1326 TTTTATA 1332
 DB 357 CTTCCTTA 351

RESULT 7
US-08-745-995A-22

; Sequence 22, Application US/08745995A

; Patent No. 6372867

; GENERAL INFORMATION:
; APPLICANT: Silver, Gary M.

; TITLE OF INVENTION: No. 637287el Serine Protease Inhibitor

; TITLE OF INVENTION: Nucleic Acid Molecules, Proteins

; NUMBER OF SEQUENCES: 41

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Heska Corporation

; STREET: 1825 Sharp Point Drive

; CITY: Fort Collins

; STATE: Colorado

; COUNTRY: USA

; ZIP: 80525

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: Windows 95

; SOFTWARE: Wordperfect for Windows, Version 7.0

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/745,995A

; FILING DATE: 07-NOV-1996

; CLASSIFICATION: 536

; ATTORNEY/AGENT INFORMATION:
; NAME: Verser, Carol Talkington

; REGISTRATION NUMBER: 37,459

; REFERENCE/DOCKET NUMBER: FC-2

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 970/493-7272

; TELEFAX: 970/484-9505

; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:

; LENGTH: 1179 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-08-745-995A-22

Query Match 9.5%; Score 132; DB 4; Length 1179;

Best Local Similarity 50.6%; Pred. No. 3.1e-27;

Matches 346; Conservative 0; Mismatches 335; Indels 3; Gaps 1;

```

Qy 652 ATCAACAATGGGTGTCATTAAGCCGAGCCGATCACCAGTGCATTCCTCGGAA 711
    |||||
Db 442 ATCAACACTGGGTGTAAGAAAATCTATACAAATATTCATGATTCATAAGCCGCT 501
    |||||
Qy 712 GCCATCATGAGCTCATCTGTTCTGCTGCTTAAACCATTTACTTCAGGGCTGTG 771
    |||||
Db 502 GATCTAGACGAGATTCAGAAATGGTTCTTGTCAATGATGTACTCAAGGGCTTTGG 561
    |||||
Qy 772 AAGTCAAGTTCAGCCCTGAGAACACAGAAAGAACTGTTCTACAGCGTATGAGAG 831
    |||||
Db 562 GAGAAACATTCAGAAAGAAACCTCAAGCAAACTTTCTATGTTTACAAATGTTGACTG 621
    |||||
Qy 832 TCGTGTTCAGCATCATGATGATGACAGGAGGAACTCCGTTATCCGGGGTGGCTGA- 890
    |||||
Db 622 ACAAAGATGATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 681
    |||||
Qy 891 --AGGCAACCCAGTGTCTGAGTGTGCTTCAAGGTGATGATCATCACCAGTGTCTCATC 948
    |||||
Db 682 TTAGATGCAAGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 741
    |||||
Qy 949 TTGCCCCAAGCTGAGAGAGCTGCGCAAGGTGAGAGAACTCACCAGAGGTGCTG 1008
    |||||
Db 742 TTGCCCCAAGCTGAGAGAGCTGCGCTCCGCTCTGAGAGAAATTAACAAATGTTGACTG 801
    |||||
Qy 1009 CAGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1068
    |||||
Db 802 CAAACCTGACTCAACGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 861
    |||||
Qy 1069 ATTGAGAGCGCTTCAGTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1128
    |||||
Db 862 ATTGATCTGAAATTAATTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 921
    |||||
Qy 1129 AGCCTGAAAGTCCAACTCCAGATATGTTGTCAGAGAGAGAGAGAGAGAGAGAGAG 1188
    |||||
Db 922 GTTCTGAGAAAGCTGATTTCAAGATGCTGAGAGATGATGATGATGATGATGATGAT 981
    |||||
Qy 1189 TCAGATGATTCATTAAGGCAATTTCTGAGGTAATGAGAGAGAGAGAGAGAGAGAGAG 1248
    |||||
Db 982 TCTAAAGTATTAAGAAAGCTTCAATTAAGTAATGAGAGAGAGAGAGAGAGAGAGAGAG 1041
    |||||
Qy 1249 AGTACCGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1308
    |||||
Db 1042 GCCACAGCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1101
    |||||
Qy 1309 AACAGGCTTTCCTGCTTTTATA 1332
    |||||
Db 1102 GAGCATCATTCCTGACTTCTTA 1125
    |||||

```

RESULT 8
US-08-745-995A-23/C
Sequence 23, Application US/08745995A
Patent No. 6372887

GENERAL INFORMATION:
APPLICANT: Silver, Gary M.
TITLE OF INVENTION: No. 6372887e1 Serine Protease Inhibitor
TITLE OF INVENTION: Nucleic Acid Molecules, Proteins
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSEE: Heeska Corporation
STREET: 1825 Sharp Point Drive
CITY: Fort Collins
STATE: Colorado
COUNTRY: USA
ZIP: 80525
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95

SOFTWARE: WordPerfect for Windows, Version 7.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/745,995A
FILING DATE: 07-NOV-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: PC-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 970/493-7272
TELEFAX: 970/484-9505
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 1179 nucleotides
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-745-995A-23

Query Match 9.5%; Score 132; DB 4; Length 1179;
Best Local Similarity 50.6%; Pred. No. 3,1e-27;
Matches 346; Conservative 0; Mismatches 335; Indels 3; Gaps 1;

```

Qy 652 ATCAACAATGGGTGTCATTAAGCCGAGCCGATCACCAGTGCATTCCTCGGAA 711
    |||||
Db 738 ATCAACACTGGGTGTAAGAAAATCTATACAAATATTCATGATTCATAAGCCGCT 679
    |||||
Qy 712 GCCATCATGAGCTCATCTGTTCTGCTGCTTAAACCATTTACTTCAGGGCTGTG 771
    |||||
Db 678 GATCTAGACGAGATTCAGAAATGGTTCTTGTCAATGATGTACTCAAGGGCTTTGG 619
    |||||
Qy 772 AAGTCAAGTTCAGCCCTGAGAACACAGAAAGAACTGTTCTACAGCGTATGAGAG 831
    |||||
Db 618 GAGAAACATTCAGAAAGAAACCTCAAGCAAACTTTCTATGTTTACAAATGTTGACTG 559
    |||||
Qy 832 TCGTGTTCAGCATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 890
    |||||
Db 558 ACAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 499
    |||||
Qy 891 --AGGCAACCCAGTGTCTGAGTGTGCTTCAAGGTGATGATCATCACCAGTGTCTCATC 948
    |||||
Db 498 TTAGATGCAAGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 439
    |||||
Qy 949 TTGCCCCAAGCTGAGAGAGCTGCGCAAGGTGAGAGAACTCACCAGAGGTGCTG 1008
    |||||
Db 438 TTGCCCCAAGCTGAGAGAGCTGCGCTCCGCTCTGAGAGAAATTAACAAATGTTGACTG 379
    |||||
Qy 1009 CAGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1068
    |||||
Db 378 CAAACCTGACTCAACGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 319
    |||||
Qy 1069 ATTGAGAGCGCTTCAGTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1128
    |||||
Db 318 ATTGATCTGAAATTAATTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 259
    |||||
Qy 1129 AGCCTGAAAGTCCAACTCCAGATATGTTGTCAGAGAGAGAGAGAGAGAGAGAGAG 1188
    |||||
Db 258 GTTCTGAGAAAGCTGATTTCAAGATGCTGTAAGAGATGATGATGATGATGATGATGAT 199
    |||||
Qy 1189 TCAGATGATTCATTAAGGCAATTTCTGAGGTAATGAGAGAGAGAGAGAGAGAGAGAG 1248
    |||||
Db 198 TCTAAAGTATTAAGAAAGCTTCAATTAAGTAATGAGAGAGAGAGAGAGAGAGAGAGAG 139
    |||||
Qy 1249 AGTACCGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1308
    |||||
Db 138 GCCACAGCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 79
    |||||
Qy 1309 AACAGGCTTTCCTGCTTTTATA 1332
    |||||
Db 78 GAGCATCATTCCTGACTTCTTA 55
    |||||

```


QY 1144 AAATCCGAGATTTGTCAGAGGCCAGATGACCTCTATGTCAGATGATTCAT 1203
 DB 1006 GACTTGTGGGCAATGTCAGGAGAG-----AGACTGTGTCTGCCAAGTTGTCAGC 1059
 QY 1204 AAGGCAATTTCTTGAGTAATGTAAGAGGCACTGAGCTGCAAGTACCGCTGTGG 1263
 DB 1060 AAGAGTTTGTGGAGGTGATGAAAGGACCGAGGCGAGCGCTGAGCTGCTTT 1119
 QY 1264 ATTGCTGGCGCTTCCGTAAACCCCAAGGAGTACTTTCAAGGCCAAGAGCCCTTCTG 1323
 DB 1120 GTAGTTGCAAGAGTCTGCAATGATCTGCCCCAGGTTCTGTCTCAACACCTTTCTT 1179
 QY 1324 GTTTTATAGAGAACTCTCTGAACTATTTATCTTCAAGGCGAG 1370
 DB 1180 TTCTTCATCAGGCAACAAGCCCAAGACATCTCTTCTGTGCGAG 1226
 RESULT 12
 US-08-385-500-3
 ; Sequence 3, Application US/08385500
 ; Patent No. 5712117
 ; GENERAL INFORMATION:
 ; APPLICANT: Sprechter, Cindy A.
 ; TITLE OF INVENTION: CYTOPLASMIC ANTIPROTEINASE-2 AND
 ; TITLE OF INVENTION: CYTOPLASMIC ANTIPROTEINASE-3 AND CODING SEQUENCES
 ; NUMBER OF SEQUENCES: 16
 ; CORRESPONDENCE ADDRESSES:
 ; ADDRESSEE: Townsend and Townsend Kourie and Crew
 ; STREET: Stewart Street Tower, One Market Plaza
 ; CITY: San Francisco
 ; STATE: California
 ; COUNTRY: US
 ; ZIP: 94105-1493
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/385,500
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Parmelee, Steven W.
 ; REGISTRATION NUMBER: 31,590
 ; REFERENCE/DOCKET NUMBER: 13952-21
 ; TELEPHONE: (206) 467-9600
 ; TELEFAX: (415) 543-5043
 ; INFORMATION FOR SEQ ID NO: 3:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1393 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: 112..1239
 ; OTHER INFORMATION: /product= "CYTOPLASMIC
 ; OTHER INFORMATION: ANTIPROTEINASE-3 PROTEIN"
 ; US-08-385-500-3
 Query Match 9.4%; Score 131; DB 1; Length 1393;
 Best Local Similarity 49.3%; Pred. No. 6.3e-27;
 Matches 437; Conservative 0; Mismatches 435; Indels 15; Gaps 3;

DB 406 CAGTTCCTCTCAACCTTTAAGGAATCTGTCTTCAATTTCTACCATGCTGAGCTGAAGAG 465
 QY 613 CTGACCTTCAAGAAATATGACAGAGCATTCAGAGCGGCATCAACAATGGGTGTCAT 672
 DB 466 CTTTCTCTTATAGAGCTGCAAGAGATTCAGAGAAACACATCAACCTGGTCTCMAAA 525
 QY 673 AAGACCGAAGGCCGAATGACCGATGTCATTCCTCGAAGCCATCAATGACTCACTGTT 732
 DB 526 AAGACCGAAGTAATGAAAGATGTTGTCGCGGTAGCTCAATGATGACGAAACAGG 585
 QY 733 CTGTGCTGTGTTAACAACATTTACTTCAAGGCGCTGTGAAAGTCAAGTTCAGCCCTGAG 792
 DB 586 CTGTTTCTTGTCAAGCATCTACTTCAAGGAAAGTAAGTAACCGTTTGAACAACA 645
 QY 793 AACACAGGAAGGAATCTGTTTACAGGCTGAGAGTGTCTGTCAGCATCTATGATG 852
 DB 646 TACACAGGAAGAAATCCCTTTAAATTAACAGAGAGAGCAAAAGCCAGTGCAGATGATG 705
 QY 853 TACACAGGAAGCAATGTCGTTATGCGCGCTGCTGAAG--GCACCGAGTCTTGAG 909
 DB 706 TATCAGAGAGCCAGCTTAAGCTCGCCACGTCGCGAGTGCAGCCAGCTGCTGAAG 765
 QY 910 TTGCTCTTCAAGGTGATGATGACATCAACATGTCCTCATCTTGCCCAAGCTGAGAAGGC 969
 DB 766 CTGCTTACGCGCAGAGAGAGAGTGAAGCTGTGCTGTGCTGCTGACAGACGCGCTGAG 825
 QY 970 CTGCGCAAGGTGAGAAAGAACTCACCCAGAGTGTGACAGAGTG-----GCTGAT 1023
 DB 826 CTCAGACGAGTGAAGAAAGTCTACTTTTGAAGAACTCACAGCCTGACCAAGCAAGCAG 885
 QY 1024 GAATTGAGAGAGATGATCTGTGTGTCACATGCCCCGCTTCCGATTGAGAGCGCTTC 1083
 DB 886 TGTATGAAGAGTACGAGGTGAAGTCTCTCCCAAAATTTAACTACAGAGATTAAT 945
 QY 1084 ACTTTGAAGAGACAGCTCCAGACATGAGGCGCTGTGCAATGCTTGAAGCCTGAAAGTCC 1143
 DB 946 GACATGGAATCTGTCTCTTGGCATTTGGAATTTGTGAGCCTTCCAAAGGCGCAAGGCT 1005
 QY 1144 AAATCCGAGATTTGTCAGAGGCCAGATGACCTCTATGTCAGATGATTCAT 1203
 DB 1006 GACTTGTGGGCAATGTCAGGAGAG-----AGACTGTGTCTGCCAAGTTGTCAGC 1059
 QY 1204 AAGGCAATTTCTTGAGTAATGTAAGAGGCACTGAGCTGCAAGTACCGCTGTGG 1263
 DB 1060 AAGAGTTTGTGGAGGTGATGAAAGGACCGAGGCGAGCGCTGAGCTGCTTT 1119
 QY 1264 ATTGCTGGCGCTTCCGTAAACCCCAAGGAGTACTTTCAAGGCCAAGAGCCCTTCTG 1323
 DB 1120 GTAGTTGCAAGAGTCTGCAATGATCTGCCCCAGGTTCTGTCTCAACACCTTTCTT 1179
 QY 1324 GTTTTATAGAGAACTCTCTGAACTATTTATCTTCAAGGCGAG 1370
 DB 1180 TTCTTCATCAGGCAACAAGCCCAAGACATCTCTTCTGTGCGAG 1226
 RESULT 13
 US-08-846-784-3
 ; Sequence 3, Application US/08846784
 ; Patent No. 5747645
 ; GENERAL INFORMATION:
 ; APPLICANT: Sprechter, Cindy A.
 ; TITLE OF INVENTION: CYTOPLASMIC ANTIPROTEINASE-2 AND
 ; TITLE OF INVENTION: CYTOPLASMIC ANTIPROTEINASE-3 AND CODING SEQUENCES
 ; NUMBER OF SEQUENCES: 16
 ; CORRESPONDENCE ADDRESSES:
 ; ADDRESSEE: Townsend and Townsend Kourie and Crew
 ; STREET: Stewart Street Tower, One Market Plaza
 ; CITY: San Francisco
 ; STATE: California
 ; COUNTRY: US
 ; ZIP: 94105-1493
 ; COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.25
 CURRENT APPLICATION NUMBER: US/08/846.784
 FILING DATE: 30-APR-1997
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/385,500
 FILING DATE: 08-FEB-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Parmelee, Steven W.
 REGISTRATION NUMBER: 31,990
 REFERENCE/DOCKET NUMBER: 13952-21
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (206) 467-9600
 TELEFAX: (415) 543-5043
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1393 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 112..1239
 OTHER INFORMATION: /product= "CYTOPLASMIC
 OTHER INFORMATION: ANTIPROTEINASE-3 PROTEIN"
 US-08-846-784-3

Query Match 9.4%; Score 131; DB 1; Length 1393;

Best Local Similarity 49.3%; Pred. No. 6.3e-27;
 Matches 437; Conservative 0; Mismatches 435; Indels 15; Gaps 3;

493 AAGCCAAATCTCTCAAGTTATGACCAATCGCTTTTGGAGACAAATCCCTT 552
 346 AAGCTGGACACAGTACTCTGTGAAACGGCCAAAGGCTCTTTGGAGAAATCTGT 405
 553 ACCTTCAATGAGACCTACAGACATCATGATGTTGATATGAGCCAAAGCTCCAGCCC 612
 406 CAGTTCCCTCAACGTTTAAAGAACTCTGCTTCAATTCACATGCTGAGCTGAAGAG 465
 613 CTGACCTTCAAGAAATGACAGAGCAATCCAGAGGCGCATCAAAATGGGTGTCAT 672
 466 CTTCTCTTATCAGAGCTGCAAGAGATCCAGAAACATCAACACCTGGGTCTCAAA 525
 673 AAGACCGAAGCCGAATCACCGATGTCAATCCCTCGAAGCCATCATGAGCTCACTGT 732
 526 AAGACCGAAGTTAAATGAAAGTGTGTCGGGTAGCTCAATGATGCAAAACAG 585
 733 CTGCTGCTGTTAACAACATTTACTTCAAGGCGCTGTGAAGTCAAGCTTCAAGCCCTGAG 792
 586 CTGCTTCTTGTCAATGACATCTTCAAGAAAGTGAATGAACCGTTTGACGAACA 645
 793 AACAACAAGAGAACTGTTCTCAAGAGCTATGAGAGTGTGTTGACATCTATGATG 852
 646 TACACAAAGGAAATGCTCTTAAATAAACCGAGAGGACAAAGCCAGTGCATGATG 705
 853 TACAGAGAGCAAGTTCGTTATCGGCGCGTGTGAAG--GCACCAAGTGTGTTAG 909
 706 TATCAGAGGCACTTTAAGTCCCAAGTGGGCGAGGTGCGGCGCAGCTGTGAG 765
 910 TTGCGCTTCAAAAGTATGATCATCAATGCTCTCATCTTGCCCAAGCTGAGAAGGC 969
 766 CTGCGCTTACGCGAGAAAGAGTGAAGCTGTGCTGTGCTGACGACGCGCTGAG 825
 970 CTGGCAAGTGTGAGAAAGAACTCAACCCAGAGGTGTGCAAGATG-----GCTGAT 1023
 826 CTCACAGCGTGAAGAAAGTCTCACTTTGAGAACTCAACGCTGGAACCAAGCCAAC 885
 1024 GAATTGAGAGATGATGCTGTGTGTCACATGCCCCCTTCGCAATTGAGAGCGGCTTC 1083

886 TGATGAAGAGTACTGAGGTTGAAGTCTCTCCAAATTAATACTAAGAGATAT 945
 1084 AGTTGAAGAGACGCTGCAAGACATGGGCTTGTGCATCTGTTACAGCCCTGAAAAGTCC 1143
 946 GACATGAATCTGTGCTTGGCATTTGGGAATGTGATGCTTCCAAACAGGGCAAGGCT 1005
 1144 AAATCCAGGTATGTTGAGAGAGCGGAGATGACCTTATGTCAGATGATTCAT 1203
 1006 GACTTGTGGCAATGTACGCGAGAG-----AGACCTGTGTCTGTCCAACTTGTGAC 1059
 1204 AAGCATTTCTTGAAGTAAATGAAGAGCAGTGAAGCAGCTGCAAGTACCGCTGTTGTG 1263
 1060 AAGAGTTTGTGAGAGTGAATGAAGAGGACCGAGGACGCGAGGGTGAAGTGTGCTT 1119
 1264 ATGCTGCGCGTGTGCTTAAACCCCAACAGGTGACTTTCAAGGCCAACAGGCTTTCTG 1323
 1120 GTAGTTCAGAGTCTGCTGATGATCTGCGCCCGAGTCTGTGTGACCAACCTTCTCT 1179
 1324 GTTTTATGAAGAGATTCCTGTAACACTATATCTTCAATGGGCGAG 1370
 1180 TTCTTCAACAGGCAACAAAGACCAACAGCATCTGTGTGTGGCAG 1226

RESULT 14

US-08-745-995A-10
 Sequence 10, Application US/08745995A
 Patent No. 6372887

GENERAL INFORMATION:
 APPLICANT: Silver, Gary M.

APPLICANT: Wisniewski, Nancy

TITLE OF INVENTION: No. 6372887e1 Serine Protease Inhibitor

TITLE OF INVENTION: Nucleic Acid Molecules, Proteins

NUMBER OF SEQUENCES: 41

CORRESPONDENCE ADDRESS:
 ADDRESS: Heska Corporation
 STREET: 1825 Sharp Point Drive
 CITY: Fort Collins
 STATE: Colorado
 COUNTRY: USA
 ZIP: 80525

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: Windows 95
 SOFTWARE: WordPerfect for Windows, Version 7.0.

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/745,995A
 FILING DATE: 07-NOV-1996

CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:
 NAME: Verser, Carol Talkington
 REGISTRATION NUMBER: 37,459
 REFERENCE/DOCKET NUMBER: FC-2

TELECOMMUNICATION INFORMATION:
 TELEPHONE: 970/493-7272

TELEFAX: 970/484-9505

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:
 LENGTH: 1197 nucleotides
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA

US-08-745-995A-10

Query Match 9.2%; Score 128.8; DB 4; Length 1197;

Best Local Similarity 51.4%; Pred. No. 2.4e-26;

Matches 323; Conservative 0; Mismatches 302; Indels 3; Gaps 1;

652 ATCAACAATGCTGTCTCAATTAAGACCGAAGCCGAATCAACGATGATTCCTCGAA 711

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Db 460 ATCAACATTGGCTTGAAGAAAACTCATGACAAAATTCATGATTGATCAAGCCGCT 519
QY 712 GCCATCAATGAGCTCACTGTTCTGTGCTGTTTAAACCATTTACTTCAAGGCGCTG 771
Db 520 GATCTAGACCAAGATTCAAGATGCTTCTGTCAATGATGATGATCAAGGCTTTGG 579
QY 772 AAGTCAAGTTTCAAGCCCTGGAACACAGAGAGAACTGTTTCAAGGCTGATGAGAG 831
Db 580 GAGAAACAATTCAAGAGAGAAACCTCAAGACAACTTCTATGTTTACTGAAACAGAG 639
QY 832 TCGTGTTCAGCATCTATGATGTATCCAGAGAGCAAGTCCGTTATCGCGCGCTGTA- 890
Db 640 ACAAGAAATGTAGAAATGATGACATTAAGCATTAATTCGTTATGAGAAATTTGAAGA 699
QY 891 --AGGACACCCAGGCTGTTGAGTTCCTTCAAGAGTGAATGATCAATCAAGTCTTATC 948
Db 700 TTATGATGCCAAGGCTGATGAAATGCTTACAGAACTCAAGATTTGGCATGTTAATCAT 759
QY 949 TTGCCCAAGCTTGAAGAGAGCTTGGCCAGGTGAGAGAGAACTCAACCCAGAGGCTG 1008
Db 760 TTGCCCAAGCAAGCAAACTGCTCTCCCGCTCTTGAAGAAAAATTAAGAAATGTTGACT 819
QY 1009 CAGAGTGGCTGATGATGATGAGAGATGATGCTGGTGGTCCAGATGCCGCTTCCG 1068
Db 820 CAAACTTACTCAAGCATGTACTCTGTGAAGTTATTTGATCTGCTTAATTTCAAG 879
QY 1069 ATTGAGAGAGGCTTCAAGTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1128
Db 880 ATTGAATCTGAATTAATTTGAATGATCTCTGAAAAAGTTGGGTATGTCGATGATGTT 939
QY 1129 AGCCCTGAAAGATCCAACTCCAGATATGTTGCAAGAGCCGAGATGACCTTATGTC 1188
Db 940 GTTCTGGAAGAACTGATTTCAAGAGATGCTGAAGATCTGATGATGATTAATTAAT 999
QY 1189 TCAGATGATTCATTAAGGATTTCTTGAAGTAAATGAAGAGAGAGAGAGAGAGAG 1248
Db 1000 TCTAAGTATTTAAAAAGCTTTCATTTGAATGAATGAAGAGAGAGAGAGAGAGAG 1059
QY 1249 AGTACCGCTGTGTGATGCTGAGCCGTT 1276
Db 1060 GCCACAGGATGTCTCATGCTTGGTTGCT 1087

RESULT 15
US-08-745-995A-11/c
; Sequence 11, Application US/08745995A
; Patent No. 6372887
; GENERAL INFORMATION:
; APPLICANT: Silver, Gary M.
; TITLE OF INVENTION: No. 6372887el Serine Protease Inhibitor
; TITLE OF INVENTION: Nucleic Acid Molecules, Proteins
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Heska Corporation
; STREET: 1825 Sharp Point Drive
; CITY: Fort Collins
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80525
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: WordPerfect for Windows, Version 7.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/745,995A
; FILING DATE: 07-NOV-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Verser, Carol Talkington
; REGISTRATION NUMBER: 37,459

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; REFERENCE/DOCKET NUMBER: FC-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 970/493-7272
; TELEFAX: 970/484-9505
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1197 nucleic acid
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-745-995A-11

Query Match 9.2%; Score 128.8; DB 4; Length 1197;
Best Local Similarity 51.4%; Pred. No. 2.4e-26;
Matches 323; Conservative 0; Mismatches 302; Indels 3; Gaps 1;

QY 652 ATCAACAAATGGGTGTCATTAAGACCGAGGCGAATCAACGATGATTCCTCGGA 711
Db 738 ATCAACACTTGGGTGAGAGAAAACTCATGCAAAATTCATGATTTGATCAAGCCGCT 679
QY 712 GCCATCAATGAGCTCACTGTTCTGTGCTGTTTAAACCATTTACTTCAAGGCGCTG 771
Db 678 GATCTAGACCAAGATTCAAGATGCTTCTGTCAATGATGATGATCAAGGCTTTGG 619
QY 772 AAGTCAAGTTTCAAGCCCTGGAACACAGAGAGAACTGTTTCAAGGCTGATGAGAG 831
Db 618 GAGAAACAATTCAAGAGAGAAACCTCAAGACAACTTCTATGTTTACTGAAACAGAG 559
QY 832 TCGTGTTCAGCATCTATGATGTATCCAGAGAGCAAGTCCGTTATCGGCGCTGTA- 890
Db 558 ACAAGAAATGTAGAAATGATGACATTAAGCATTAATTCGTTATGAGAAATTTGAAGA 499
QY 891 --AGGACACCCAGGCTGTTGAGTTCCTTCAAGAGTGAATGATCAATCAAGTCTTATC 948
Db 498 TTATGATGCCAAGGCTGATGAAATGCTTACAGAGAACTCAAGATTTGGCATGTTAATCAT 439
QY 949 TTGCCCAAGCTTGAAGAGAGCTTGGCCAGGTGAGAGAGAGAGAGAGAGAGAGAGAG 1008
Db 438 TTGCCCAAGCAAGCAAACTGCTCTCCCGCTCTTGAAGAAAAATTAAGAAATGTTGACT 379
QY 1009 CAGAGTGGCTGATGATGATGAGAGAGATGATGCTGTGTCACATGCGCCGCTTCCG 1068
Db 378 CAAACTTACTCAAGCATGTACTCTGTGAAGTTATTTGATCTGCTTAATTTCAAG 319
QY 1069 ATTGAGAGAGGCTTCAAGTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1128
Db 318 ATTGATCTGAATTAATTTGAATGATCTCTGAAAAAGTTGGGTATGTCGATGATGTT 259
QY 1129 AGCCCTGAAAGATCCAACTCCAGATATGTTGCAAGAGCCGAGATGACCTTATGTC 1188
Db 258 GTTCTGGAAGAACTGATTTCAAGAGATGCTGAAGATCTGATGATGATTAATTAAT 199
QY 1189 TCAGATGATTCATTAAGGATTTCTTGAAGTAAATGAAGAGAGAGAGAGAGAGAGAG 1248
Db 198 TCTAAGTATTTAAAAAGCTTTCATTTGAATGAATGAAGAGAGAGAGAGAGAGAGAG 139
QY 1249 AGTACCGCTGTGTGATGCTGAGCCGTT 1276
Db 138 GCCACAGGATGTCTCATGCTTGGTTGCT 111

Search completed: June 27, 2003, 00:10:45
Job time : 217 secs

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| 999-8157 | Sequence 8157, <i>Ap</i> |
| -761-31366 | Sequence 31366, <i>P</i> |
| -352-4934 | Sequence 4934, <i>Ap</i> |
| -352-9353 | Sequence 9353, <i>Ap</i> |
| -352-10797 | Sequence 10797, <i>Ap</i> |
| -352-2262 | Sequence 2262, <i>Ap</i> |
| -352-3191 | Sequence 3191, <i>Ap</i> |
| -352-4443 | Sequence 4443, <i>Ap</i> |
| -352-7749 | Sequence 7749, <i>Ap</i> |
| -352-3996 | Sequence 3996, <i>Ap</i> |
| -352-5899 | Sequence 5899, <i>Ap</i> |
| -352-14625 | Sequence 14625, <i>Ap</i> |
| -352-10061 | Sequence 10061, <i>P</i> |
| -352-8821 | Sequence 8821, <i>Ap</i> |
| 999-8263 | Sequence 8263, <i>Ap</i> |
| -352-3190 | Sequence 3190, <i>Ap</i> |
| -352-2260 | Sequence 2260, <i>Ap</i> |

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| 20 | 276.2 | 19.8 | 361 | 10 | US-09-960-352-2748 | Sequence 2748, Ap |
| 21 | 276.2 | 19.8 | 423 | 10 | US-09-960-352-12011 | Sequence 12011, Ap |
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| 23 | 264.4 | 19.0 | 414 | 10 | US-09-960-352-8537 | Sequence 8507, Ap |
| 24 | 264 | 18.9 | 425 | 10 | US-09-960-352-888 | Sequence 888, App |
| 25 | 258 | 18.5 | 410 | 9 | US-09-918-995-7912 | Sequence 7912, Ap |
| 26 | 254 | 18.2 | 355 | 10 | US-09-980-107-11580 | Sequence 1580, Ap |
| 27 | 253.4 | 18.2 | 429 | 10 | US-09-960-352-6810 | Sequence 6810, Ap |
| 28 | 253 | 18.1 | 395 | 9 | US-09-918-995-7606 | Sequence 7606, Ap |
| 29 | 253 | 18.1 | 401 | 10 | US-09-960-352-11087 | Sequence 1087, Ap |
| 30 | 248.2 | 17.8 | 391 | 10 | US-09-960-352-11868 | Sequence 11868, Ap |
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| 32 | 243 | 17.4 | 416 | 10 | US-09-960-352-4656 | Sequence 4656, Ap |
| 33 | 240.6 | 17.2 | 410 | 10 | US-09-960-352-14810 | Sequence 14810, Ap |
| 34 | 239 | 17.1 | 387 | 10 | US-09-960-352-10294 | Sequence 10294, Ap |
| 35 | 238.4 | 17.1 | 400 | 10 | US-09-960-352-3253 | Sequence 3253, Ap |
| 36 | 235.2 | 16.9 | 398 | 10 | US-09-960-352-7553 | Sequence 7553, Ap |
| 37 | 185.6 | 13.3 | 322 | 10 | US-09-960-352-3472 | Sequence 3472, Ap |
| 38 | 178.2 | 12.8 | 267 | 10 | US-09-880-107-2110 | Sequence 2130, Ap |
| 39 | 178.2 | 12.8 | 334 | 10 | US-09-880-107-2294 | Sequence 2294, Ap |
| 40 | 154.2 | 11.1 | 337 | 10 | US-09-960-352-11040 | Sequence 11040, Ap |
| 41 | 126.2 | 9.0 | 1476 | 9 | US-09-974-298-54 | Sequence 94, Ap1 |
| 42 | 119 | 8.5 | 235 | 10 | US-09-960-352-14147 | Sequence 14147, Ap |
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| 44 | 118 | 8.5 | 1331 | 10 | US-09-925-301-358 | Sequence 358, App |
| 45 | 118 | 8.5 | 1933 | 10 | US-09-960-352-11778 | Sequence 11778, Ap |

ALIGNMENTS

ULT 1
09-828-592-6

sequence 6, Application US
 Patent No. US20010055591A1

GENERAL INFORMATION:
APPLICANT: Walston, Timothy
ADDRESS: 6100
CITY: 6100

APPLICANT: cooper, scott
APPLICANT: Rezaie, Alireza
APPLICANT: Rezaie, Alireza

FILE REFERENCE: 7869.10USU1
 TITLE OF INVENTION: ANTI-HROMBIN H-HELIX
 PRIORITY APPLICATION NUMBER: US/A9/838 583

CURRENT FILING DATE: 2001-04-06
CURRENT APPLICATION NUMBER: 60/195 873

NUMBER OF SEQ ID NOS: 16

SOFTWARE: PatentIn Ver. 2.1
EO ID NO 6

LENGTH: 1395
TYPE: DNA

ORGANISM: Homo sapiens
09-828-592-6

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Query Match      100.0%; Score 1395; DB 10; Length 1395
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Test Local Similarity 100.0%; Pred. No. 0;
Matches 1395; Conservative 0; Mismatches 0; Indels 0; Gaps 0

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1 ATGATATCCAA TGTAGTA GAACTGA AACTCTG GAAAAGG AAGCTTAT CTTTGTCC

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121 ACAGCCAAGCCGGGACATTCATGAATCCATGATTCATTTACCGCTCCCGGAGAG

121 ACAGCCAAGCGCGGACATTCCCATGATCCCATGTGCATTACCGCTCCCCGGAGAAG ;

181 AAGGCACTGAGGATGAGGCTCAGAACAGAGATCCCGGAGGCCACCAACCGCGTGC 2

181 AAGGCACTGAGGATGAGGCTCAGAACGAGAAGATCCCGGAGGCCACCAACCGGCGTGC ;

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| OY | 241 | IGGGAGCACTGCCAAGGCCAATTCGCGCTTGCTACACCTTCTATCAGACCTGGCAAT | 300 |
| Db | 241 | TGGGAACGTCCAAAGGCCAATTCGCGCTTGCTACACCTTCTATCAGACCTGGCAAT | 300 |
| OY | 301 | TCCAAGATGACAAATGATACATTTCCGTGCACCCCTGAGATCTCCACGGCTTTGCT | 360 |
| Db | 301 | TCCAAGATGACAAATGATACATTTCCGTGCACCCCTGAGATCTCCACGGCTTTGCT | 360 |
| OY | 361 | ATGACCAAGCTGGGTGCTGTATGACACCTCCAGCACTGATGGAGATATTTAAGTTT | 420 |
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| OY | 421 | GACACCAATCTGAGAAAACATCTGATGAGATCCACTTCTTTGCCAACTGAACCTGC | 480 |
| Db | 421 | GACACCAATCTGAGAAAACATCTGATGAGATCCACTTCTTTGCCAACTGAACCTGC | 480 |
| OY | 481 | CGACTCTATCGAAAAGCCAAACAAATCCTCAAGTAGATGACCAATCGACTTTTGGAA | 540 |
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| OY | 541 | GACAAATCCCTTACCTTCAATGAGACCTACAGACATCAGTGAGTTGTATATGAGACC | 600 |
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| OY | 781 | TTACAGCCCTGAGAACACAAAGGAAGAACTGTTCTACAGGCTGATGAGAGATCGTGTCCA | 840 |
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| OY | 841 | GCATTTATGATGTATACAGAAAGGCAAGTTCCGTTATCGGCGCGGTGGCGAAGGCCACCGAG | 900 |
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| OY | 901 | GTGCTTGAAGTTGCCCTTCAAAAGGTATGACATCACATGATCTTCAATCTTCCCAAGCCT | 960 |
| Db | 901 | GTGCTTGAAGTTGCCCTTCAAAAGGTATGACATCACATGATCTTCAATCTTCCCAAGCCT | 960 |
| OY | 961 | GAGAAAGACCTGGGCCAAGGTGGAGAAAGAACTCACCCAGAGGTCTGACAGAGTGGCTTG | 1020 |
| Db | 961 | GAGAAAGACCTGGGCCAAGGTGGAGAAAGAACTCACCCAGAGGTCTGACAGAGTGGCTTG | 1020 |
| OY | 1021 | GATGAATTTGAGGAATGATGTTGGTGGTCCACATGCCCGCTTCCGAGTTGAGGAGCGGC | 1080 |
| Db | 1021 | GATGAATTTGAGGAATGATGTTGGTGGTCCACATGCCCGCTTCCGAGTTGAGGAGCGGC | 1080 |
| OY | 1081 | TTCACTTTGAAGAGACAGCTGCAACATGAGGCTTGTGATCTGTTCAGCCCTGAAAAG | 1140 |
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| OY | 1141 | TTCAAACTCCAGGATATTGTTCAGAGAGGCCGAGATGACCTTATGTCTCAGATGCAATTC | 1200 |
| Db | 1141 | TTCAAACTCCAGGATATTGTTCAGAGAGGCCGAGATGACCTTATGTCTCAGATGCAATTC | 1200 |
| OY | 1201 | CATTAAGCATTTCTTGAGGTAAATGAAGGCACTGAAGCAGCTGCAAGTACGCTGTT | 1260 |
| Db | 1201 | CATTAAGCATTTCTTGAGGTAAATGAAGGCACTGAAGCAGCTGCAAGTACGCTGTT | 1260 |
| OY | 1261 | GTGATTTGTGGCCGCTTTCCTTAAACCCCAACAGGGTGACTTTTCAAGGCCAACAGGCTTTTC | 1320 |
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| OY | 1321 | CTGCTTTTATTAAGAAAGTTCTCTGTGAACATAATTAATCTTCAATGAGGAGATGACCAAC | 1380 |

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| Db | 1321 | CTGCTTTTATTAAGAGAAGTTCCTCTGAACCTATATCTTCATGGGCAGAGTACCCAC | 1380 |
| Qy | 1381 | CCTGTGTAACTAA | 1395 |
| Db | 1381 | CCTGTGTAACTAA | 1395 |

RESULT 2
US-09-864-761-14838
; Sequence 14838, Application US/09864761
; Patent No. US20020048763A1
; Current Information

GENERAL INFORMATION:
APPLICANT: Penn, Sharon G.
APPLICANT: Rank, David R.
APPLICANT: Rankel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Aeomica-X-1

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|---------------------------|--------|---------------------|-----------|-------------|
| Query Match | 28.5% | Score 397.4; | DB 10; | Length 578; |
| Best Local Similarity | 98.5%; | Pred. No. 1.7e-119; | | |
| Matches 401; Conservative | 0; | Mismatches 6; | Indels 0; | Gaps 0; |

Oy 751 ATTACTTCAAGGCGCTGTGGAAGTCAAAAGTTACAGCCCTGAGAACACAAAGAGAACTG 810
Db 125 ATTCTTTCAAGGCGCTGTGGAAGTCAAAAGTTACAGCCCTGAGAACACAAAGAGAACTG 184
Oy 811 TTCTACAAGGCTGTGAGAGTGTGTTACAGATCTATGATGTACAGAGAGGCAAGTTT 870
Db 185 TTCTACAAGGCTGTGAGAGTGTGTTACAGATCTATGATGTACAGAGAGGCAAGTTT 244
Oy 871 CGTTATCGGCGCGTGTGGAAGGCAAGGCTGTGAGTTGCTTCAAGAGTGTATAC 930
Db 245 CGTTATCGGCGCGTGTGGAAGGCAAGGCTGTGAGTTGCTTCAAGAGTGTATAC 304
Oy 931 ATCAACCATGCTCTCATCTTGCCCAAGCTGAGAGAGGCTGAGGCAAGTGAAGAA 990
Db 305 ATCAACCATGCTCTCATCTTGCCCAAGCTGAGAGAGGCTGAGGCAAGTGAAGAA 364
Oy 991 CTCACCCGAGAGTGTCTCAAGAGTGTGATGATGAGAGAGATGATGCTGTGTC 1050
Db 365 CTCACCCGAGAGTGTCTCAAGAGTGTGATGATGAGAGAGATGATGCTGTGTC 424
Oy 1051 CACATGCGCGCTTCCGATTTGAGAGAGGCTTCAATTGGAAGAGACCTGCAAGACTG 1110
Db 425 CACATGCGCGCTTCCGATTTGAGAGAGGCTTCAATTGGAAGAGACCTGCAAGACTG 484
Oy 1111 GACCTTGTGATCTGTGAGGCGCTGAGAAAGTCCAAACTCCAGGAT 1157
Db 485 GACCTTGTGATCTGTGAGGCGCTGAGAAAGTCCAAACTCCAGGAT 531

RESULT 3

US-09-918-995-8157
; Sequence 8157, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO: 8157
; LENGTH: 418
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-918-995-8157

Query Match 28.3%; Score 394.2; DB 9; Length 418;
Best Local Similarity 97.9%; Pred. No. 1.5e-118;
Matches 410; Conservative 0; Mismatches 8; Indels 1; Gaps 1;

Oy 787 CCTGGAACACAAAGGAAGTCTTCTACAAGGCTGATGAGAGTCCGTTGACACATCT 846
Db 1 CCTGGAACACAAAGGAAGTCTTCTACAAGGCTGATGAGAGTCCGTTGACACATCT 60
Oy 847 ATGATGTACAGGAAGGCAAGTTCGTTATCGGCGCTGTGAAAGGCAACCAAGTGTCT 906
Db 61 ATGATGTACAGGAAGGCAAGTTCGTTATCGGCGCTGTGAAAGGCAACCAAGTGTCT 120
Oy 907 GAGTTGCCCTTTCAAGGCTGATGATCAACATGCTCTCATCTTGGCCCAAGCTTGAAG 966
Db 121 GAGTTGCCCTTTCAAGGCTGATGATCAACATGCTCTCATCTTGGCCCAAGCTTGAAG 180
Oy 967 AGCCTGCAAGAGTGTGAGAGAGTCAACCCAGAGGCTGTGAGAGAGTGTGATGAA 1026
Db 181 AGCCTGCAAGAGTGTGAGAGAGTCAACCCAGAGGCTGTGAGAGAGTGTGATGAA 240
Oy 1027 TTGAGAGAGATGATCTGTGTGTCACATGCCCGCTTCCGATTGAGAGCGGCTTCAGT 1086
Db 1027 TTGAGAGAGATGATCTGTGTGTCACATGCCCGCTTCCGATTGAGAGCGGCTTCAGT 1086

Db 241 TTGAGAGAGATGATCTGTGTGTCACATGCCCGCTTCCGATTGAGAGCGGCTTCAGT 300
Oy 1087 TTGAGAGAGAGTGTGAGAGATGATGAGAGTGTGATCTGTGACCCCTGAAAGTCCAA 1146
Db 301 TTGAAAGAGAGTGTGAGAGATGAGAGAGTGTGATCTGTGACCCCTGAAAGTCCAA 359
Oy 1147 CTCCAGATATTTGTCAGAGAGCGGAGATGATGATCTTATGCTGATGATTCATTA 1205
Db 360 CTCCAGATATTTGTCAGAGAGCGGAGATGATGATCTTATGCTGATGATTCATTA 418

RESULT 4

US-09-864-761-31366
; Sequence 31366, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263,6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO: 31366
; LENGTH: 395
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AL136170.2
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 30
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 12
; OTHER INFORMATION: SWISSPROT HIT: P01008, EVALUATE 4.00e-72
; OTHER INFORMATION: NT HIT: g111422599, EVALUATE 0.00e+00


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RESULT 7
US-09-960-352-10797
; Sequence 10797, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengping
; APPLICANT: Byatt, John C.
; APPLICANT: Mathialagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; FILE REFERENCE: 16511.006/37-21(10298)C
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 10797
; LENGTH: 422
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 46-LIB34-037-Q1-E1-D6
US-09-960-352-10797

Query Match      24.1%; Score 336.4; DB 10; Length 422;
Best Local Similarity 88.8%; Pred. No. 1.4e-99;
Matches 364; Conservative 0; Mismatches 46; Indels 0; Gaps 0;

QY 613 CTGACCTCAAGGAATGACAGCAATCCAGAGGCGCATCAACAATGGGTTCAT 672
DB 13 CTGACCTCAAGGAATGACAGCAATCCAGAGGCGCATCAACAATGGGTTCAT 72
QY 673 AAGACCGAAGCCGATACCGATGATGATGATGATGATGATGATGATGATGAT 732
DB 73 AAGACCGAAGCCGATACCGATGATGATGATGATGATGATGATGATGATGAT 132
QY 733 CTGTCGTGCTTACCACTTACTTCAAGGCGCTGTGGAAGTCAAGTTCAGCCTGAG 792
DB 133 CTGTCGTGCTTACCACTTACTTCAAGGCGCTGTGGAAGTCAAGTTCAGCCTGAG 192
QY 793 AACCAAGGAAGGAATGCTGTTCAGAGGCTGATGAGAGTGTGTCAGCATCTATGATG 852
DB 193 AACCAAGGAAGGAATGCTGTTCAGAGGCTGATGAGAGTGTGTCAGCATCTATGATG 252
QY 853 TACCAAGGAAGGAATGCTGTTCAGAGGCTGATGAGAGTGTGTCAGCATCTATGATG 912
DB 253 TACCAAGGAAGGAATGCTGTTCAGAGGCTGATGAGAGTGTGTCAGCATCTATGATG 312
QY 913 CCCTTCAAGGTGATGATCATCATCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTG 972
DB 313 CCCTTCAAGGTGATGATCATCATCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTG 372
QY 973 GCCAAGGTGGAAGGAATGCTCAAGGCTGAGAGTGTGCTGGA 1022
DB 373 GCCAAGGTGGAAGGAATGCTCAAGGCTGAGAGTGTGCTGGA 422

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; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 10-LIB34-023-Q1-E1-C5
US-09-960-352-2262

Query Match      24.0%; Score 334.4; DB 10; Length 418;
Best Local Similarity 90.3%; Pred. No. 6.3e-99;
Matches 362; Conservative 0; Mismatches 46; Indels 0; Gaps 0;

QY 488 ATCGAAGGAAGGAATGCTGTTCAGAGGCTGATGAGAGTGTGTCAGCATCTATGATG 547
DB 11 ATCGAAGGAAGGAATGCTGTTCAGAGGCTGATGAGAGTGTGTCAGCATCTATGATG 70
QY 548 CCCTTCAAGGTGATGATCATCATCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTG 607
DB 71 CCCTTCAAGGTGATGATCATCATCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTG 130
QY 608 AGCCCTGACTTCAAGGAATGCAAGCAATCCAGAGGCGCATCAACAATGGGTGT 667
DB 131 AGCCCTGACTTCAAGGAATGCAAGCAATCCAGAGGCGCATCAACAATGGGTGT 190
QY 668 CCATTAAGACCGAAGGCGCATCAAGCAATCCAGAGGCGCATCAACAATGGGTGT 727
DB 191 CCATTAAGACCGAAGGCGCATCAAGCAATCCAGAGGCGCATCAACAATGGGTGT 250
QY 728 CTGTCGTGCTGCTGCTTACCACTTACTTCAAGGCGCTGTGGAAGTCAAGTTCAGC 787
DB 251 CTGTCGTGCTGCTGCTTACCACTTACTTCAAGGCGCTGTGGAAGTCAAGTTCAGC 310
QY 788 CTGGAACACAGGAAGGAATGCTGTTCAGAGGCTGATGAGAGTGTGTCAGCATCTA 847
DB 311 CTGGAACACAGGAAGGAATGCTGTTCAGAGGCTGATGAGAGTGTGTCAGCATCTA 370
QY 848 TGATGTCACAGGAAGGAATGCTGTTCAGAGGCTGATGAGAGTGTGTCAGCATCTA 895
DB 371 TGATGTCACAGGAAGGAATGCTGTTCAGAGGCTGATGAGAGTGTGTCAGCATCTA 418

RESULT 9
US-09-960-352-3191
; Sequence 3191, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengping
; APPLICANT: Byatt, John C.
; APPLICANT: Mathialagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; FILE REFERENCE: 16511.006/37-21(10298)C
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 3191
; LENGTH: 384
; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 14-LIB34-011-Q1-E1-D5
US-09-960-352-3191

Query Match      23.1%; Score 322.8; DB 10; Length 384;
Best Local Similarity 90.3%; Pred. No. 3.8e-95;
Matches 345; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

QY 324 TTTCCTGTACCCCTGATGATCTCAAGGCTTTTGTCTATGACCAAGCTGGTGTGTA 383
DB 2 TTTCCTGTACCCCTGATGATCTCAAGGCTTTTGTCTATGACCAAGCTGGTGTGTA 61
QY 384 TGAACCTCAGAGAGTGAAGTATTTAAGTTGACCAAGCTGATCTGGAAGCAATC 443
DB 62 TGAACCTCAGAGAGTGAAGTATTTAAGTTGACCAAGCTGATCTGGAAGCAATC 121
QY 444 TGATGATCCACTTCTTCTTGTGCAACTGACCTGATGCAAGCAAGCAAGCA 503

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Db 122 TGATGATCCACTTTTCTTCCAACTGACCTCTATGAAAAAACCATA 181
Oy 504 ATCTCCAGATTAGTATCAGCCATCGCTTTTGGAGACAAATCCCTTACCTTCANTGA 563
Db 182 ATCTCTGAGTTGGTATCAGCCACCGTCTTTTGGAGACAAATCATTCATTCATGA 241
Oy 564 GACCTACAGAGATCATGAGTTGGTATATGAGCCAAAGCTCCAGCCCTTGACTTCA 623
Db 242 GACCTACAGAGATCATGAGTTGGTATATGAGCCAAAGCTCCAGCCCTTGACTTCA 301
Oy 624 GGAATATGAGAGCATCCAGAGCGGCTCAACAAATGGTGTCAATTAAGCCGAGG 683
Db 302 GGAATATGAGAGCATCCAGAGCTCAAGATTGACTATCAACATGATATCAATTAAGCTGAAG 361
Oy 684 CCGAATCAGCATGTCATTTCC 705
Db 362 GCGTATCAGCATGTCATTTCC 383

RESULT 10

US-09-960-352-4443
; Sequence 4443, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengbing
; APPLICANT: Byatt, John C.
; APPLICANT: Mathialagan, Nagappan
; TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
; FILE REFERENCE: 16511.006/37-21(10298)C
; CURRENT APPLICATION NUMBER: US/09/960,352
; NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 4443
; LENGTH: 408
; TYPE: DNA
; ORGANISM: Bos taurus
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (330)
; OTHER INFORMATION: unsure at all n locations
; OTHER INFORMATION: Clone ID: 19-LIB34-048-01-E1-E3
US-09-960-352-4443

Query Match 23.1%; Score 321.8; DB 10; Length 408;
Best Local Similarity 86.9%; Pred. No. 8.4e-95;
Matches 353; Conservative 0; Mismatches 53; Indels 0; Gaps 0;

Oy 624 GGAATATGAGAGCATCCAGAGCGGCTCAACAAATGGTGTCAATTAAGCCGAGG 683
Db 1 GGAATATGAGAGCATCCAGATTGACTATCAACATGATATCAATTAAGCTTCAAGG 60
Oy 684 CCGAATCAGCATGTCATTTCCGAGAGCCATCATGAGTCACATGTCGTGGTGTG 743
Db 61 GCGTATCAGTATGATCTATTCCTCCAGAGCCATCAATTAAGTTCATGTCGTGGTGTG 120
Oy 744 TAACACATTTACTTCAAGGCGCTGTGAAGTCAAAATTCAGCCCTGAGAACACAGAA 803
Db 121 CAACACATTTACTTCAAGGCGCTGTGAAGTCAAAATTCAGTCCGAGAACACAGAA 180
Oy 804 GGAATGTTTCTACAGGCGCTGTGAAGTCTGTTCAGCATCTATGATGATACAGAGG 863
Db 181 GGAATGTTTCTACAGGCGCTGTGAAGTCTGTTCAGCATCTATGATGATACAGAGG 240
Oy 864 CAAGTCCGTTATCGGCGGTGTGAAGGCAACGAGTCTGAGTGTCCCTTCAAGG 923
Db 241 CAAGTCCGTTATCGGAGTACAGAGACACAGGCTGTGAAGTCTTCAAGG 300
Oy 924 TGATGATCAGCATGTCATTTCCGAGAGCGCTGAGAGAGCGCTGAGAGGCTGAG 983
Db 301 TGATGATCAGCATGTCATTTCCGAGAGCGCTGAGAGAGCGCTGAGAGGCTGAG 360

Oy 984 GAGGACTCACCCGAGAGTGTGTCAGAGATGCTGATGATG 1029
Db 361 ACAGGACTCACCCGAGAGATGCTGAGAGGCTGATGATG 406

RESULT 11

US-09-960-352-7749
; Sequence 7749, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengbing
; APPLICANT: Byatt, John C.
; APPLICANT: Mathialagan, Nagappan
; TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
; FILE REFERENCE: 16511.006/37-21(10298)C
; CURRENT APPLICATION NUMBER: US/09/960,352
; NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 7749
; LENGTH: 388
; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 33-LIB34-033-Q1-E1-A2
US-09-960-352-7749

Query Match 22.7%; Score 316; DB 10; Length 388;
Best Local Similarity 88.4%; Pred. No. 6.5e-93;
Matches 343; Conservative 0; Mismatches 45; Indels 0; Gaps 0;

Oy 282 CTATGAGCAGCTGGCAGATTCAGAGATGACATATATATTTCTGTCAACCCCTGAG 341
Db 1 CTATGAGCAGTTGGCAGACTCCAGATTAACATATACAAATTTCTGTCAACCCCTGAG 60
Oy 342 TATCTCCAGCGCTTTGATGAGACCAAGCTGGGTCTGTATGACACCCCTCCAGACT 401
Db 61 TATCTCCAGCGTTTGTGATGAGACCAAGCTGGGTCTGTGACCAAGCTGATGACAGAT 120
Oy 402 GATGAGGATTTAAGTTGACACCATATCTGAGAAAATCTGTGATGATGATCACTTT 461
Db 121 GATGAGGATTTAAGTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 180
Oy 462 CTTTGCCAACTGAACTGCGACTTATGAGAAAGCCAAATCTCTCAAGTTGATG 521
Db 181 CTTTGCCAACTGAACTGCGACTTATGAGAAAGCCAAATCTCTCAAGTTGATG 240
Oy 522 AGCAATGCGCTTTTGGAGCAATCCCTTACTTCAATGAGACTACAGAGATGAG 581
Db 241 AGCAATGCGCTTTTGGAGCAATCCCTTACTTCAATGAGACTACAGAGATGAG 300
Oy 582 TGAGTTGATATGAGCCAGCTCCAGCCCTGAGTCTTCAAGAAAATGAGAGCAATC 641
Db 301 TGAGTTGATATGAGCCAGCTCCAGCCCTGAGTCTTCAAGAAAATGAGAGCAATC 360
Oy 642 CAGAGCGCATCAACAAATGGTGTCC 669
Db 361 TAGATTGATATCAACAAATGATATCC 388

RESULT 12
US-09-960-352-3996
; Sequence 3996, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengbing
; APPLICANT: Byatt, John C.
; APPLICANT: Mathialagan, Nagappan
; TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
; FILE REFERENCE: 16511.006/37-21(10298)C
; CURRENT APPLICATION NUMBER: US/09/960,352

| | | | | | | | | |
|----|-----------------------|---|---|-------------|------------|----|--------|-----|
| | Query Match | 22.5% | Score | 314.4 | DB | 10 | Length | 400 |
| | Best Local Similarity | 88.2% | Pred. | No. 2.2e-92 | | | | |
| | Matches | 353 | Conservative | 0 | Mismatches | 46 | Indels | 1 |
| Gy | | | | | | | | |
| | 714 | CATCAATGAGCTCACTGTTTCGGTGTGTAAACCATTTACTTCAAGGGCCCTTGCGAA | | | | | | 773 |
| | | | | | | | | |
| Dδ | | 1 | CACCATATAGTTCACTGCCTGTGTGTGTATCAACACATTTCCTTAAGGGCCCTTGCGAA | | | | | 60 |
| Oy | | | | | | | | |
| | 774 | GTCAAAGTTCAAGCCCTGAAGAACAAGGAAGCAACCTGTTCTTCAAGGCTGATGAGAGTTC | | | | | | 833 |

| | Query Match | 22.3% | Score | 311.6 | DB | 10 | Length | 368 |
|----|-----------------------|--|----------------------------|---------|------------|----|--------|-----|
| | Best Local Similarity | 90.7% | Pred. No. | 1.7e-91 | | | | |
| | Matches | 332 | Conservative | 0 | Mismatches | 34 | Indels | 0 |
| QY | 433 | GAGAAAACATCTGATCAGATCCACTTCTTCTTGGCAAC | CTGAACTGACGCGCACTATCGA | 492 | | | | |
| DB | 3 | GAGAAAACCTTGATCAGATCCACTTTTCTTGGCAAC | CTGAACTGACGCGCACTATCGA | 62 | | | | |
| QY | 493 | AAAGCCACAATACTCTCCAACTTATGATCAGCCAA | TGCGCTTTTGGAGACAAATCCCTT | 552 | | | | |
| DB | 63 | AAAGCCAAATAATCCTCTGAGTTGGTATCAGCCAA | CCGCTTTTGGAGACAAATCCATT | 122 | | | | |
| QY | 553 | AACCTTCATGAGACCTACAGAGCACTCAGTGA | CTGTATATGAGGCCAAGCTCCAGGCC | 612 | | | | |
| DB | 123 | ACATTCAATGAGACCTTACAGAGCACTCAGTGA | TGTATATGAGGCCAAGCTCCAGGCC | 182 | | | | |
| QY | 613 | CTGCACTTCAAGAAATAATGACAGCAATTCAGAGCGGC | CCATCAACAAATGSGTGTCCAA | 672 | | | | |
| DB | 183 | CTGCACTTCAAGAGGAAATGACAGAGATTCAGATT | CACTATACCAATGSAATATCCAA | 242 | | | | |
| QY | 673 | AAGACCGAAGGCCGAATACCGATGCAATTCCTCGAA | AGCCATCAATGAGTCACTGTT | 732 | | | | |
| DB | 243 | AAGACGTAAGGGCGTATCACTGATGTCAATCCCC | CAAGCCATCAATGAGTTCACTGTC | 302 | | | | |
| QY | 733 | CTGGTGTCTGTTAAACCACTTTACTTCAAGGGCCT | GTGGAAGTCAAAGTTCAAGCCTTGA | 792 | | | | |
| DB | 303 | CTGGTGTCTGTTAAACCACTTTACTTCAAGGGCCT | GTGGAAGTCAAAGTTCAAGCCTTGA | 362 | | | | |

QY 793 AACACA 798
|||
Db 363 AACACA 368

RESULT 15
US-09-960-352-10061
; Sequence 10061, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengbing
; APPLICANT: Byatt, John C.
; APPLICANT: Mathialagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
; FILE REFERENCE: 16511.006/37-21(10298)C
; CURRENT APPLICATION NUMBER: US/09/960,352
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 10061
; LENGTH: 357
; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 43-LIB34-023-Q1-E1-C4
US-09-960-352-10061

Query Match 20.8%; Score 289.8; DB 10; Length 357;
Best Local Similarity 88.2%; Pred. No. 2.4e-84;
Matches 315; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

QY 519 ATCAGCCAAATCGCCTTTTGGAGACAATCCCTTCAATGAGACCTACCGAGACAT 578
|||
Db 1 ATAGGCCAACCGTCTTTTGGAGACAATCCCTTCAATGAGACCTACCGAGACAT 60
QY 579 CAGTGAGTTGATATGAGAGCCCAAGCTCCAGCCCCCTGAGCTTCAAGAAAATGCAGACA 638
|||
Db 61 CAGTGACGTGATATGAGAGCCCAAGCTCCAGCCCCCTGAGCTTCAAGAAAATGCAGACA 120
QY 639 ATCCAGAGGCGGCATCAACAATGGGTGTCCATAAAGCCGAGCCGATCAGCATGT 698
|||
Db 121 GTCCAAATGATATCAACCAATGATATCAATTAAGACTGAAGGCGTATCATGT 180
QY 699 CATTCCTCGGAAGCCATCATGAGCTCACTGTCTGTGCTGTGTTAACAACATTTACTT 758
|||
Db 181 CATTCCTCGGAAGCCATCATGAGCTCACTGTCTGTGCTGTGTTAACAACATTTACTT 240
QY 759 CAAGGCGCTGTGAAATCAAGTTCAAGCCCTGAGAAACAAGAAAGAACTGTTTCAAA 818
|||
Db 241 CAAGGCGCTGTGAAATCAAGTTCAAGCCCTGAGAAACAAGAAAGAACTGTTTCAAA 300
QY 819 GCGTGATGAGAGTCTGTTTCAAGATCATATGATGTAACAGGAAGCAAGTTCGTTA 875
|||
Db 301 GCGTGATGAGAGTCTGTTTCAAGATCATATGATGTAACAGGAAGCAAGTTCGTTA 357

Search completed: June 27, 2003, 00:14:48
Job time : 232 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 26, 2003, 16:21:51 ; Search time 1899 Seconds
(without alignments)
11897.159 Million cell updates/sec

Title: US-09-828-592-6
Perfect score: 1395

Sequence: 1 atgattccatgcgatgagtag.....ccaacctgtgtgaagtaa 1395

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estcov:*
6: em_estcpl:*
7: em_estro:*
8: em_hic:*
9: gb_est1:*
10: gb_est2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estcom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_trod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|--------|-------------|--------|-------|--------------------|
| 1 | 1391.8 | 99.8 | 1794 | 11 | AF130100 Homo sapi |
| 2 | 1017.6 | 72.9 | 1510 | 11 | BC011165 Mus muscu |
| 3 | 742.2 | 53.2 | 831 | 9 | AL532135 AL532135 |
| 4 | 733.6 | 52.6 | 826 | 9 | AL564291 AL564291 |
| 5 | 695 | 49.8 | 728 | 12 | BG564415 BG564415 |
| 6 | 666 | 47.7 | 666 | 9 | AI207425 HA2767 Hu |

| 7 | 661.4 | 47.4 | 817 | 12 | BG567696 |
|----|-------|------|-----|----|----------|
| 8 | 653.8 | 46.9 | 725 | 10 | AV653910 |
| 9 | 650.8 | 46.7 | 905 | 9 | AI255692 |
| 10 | 646 | 46.3 | 882 | 13 | BI145342 |
| 11 | 635.2 | 45.5 | 852 | 12 | BG569095 |
| 12 | 634.6 | 45.5 | 675 | 10 | AV682065 |
| 13 | 628.2 | 45.0 | 744 | 12 | BG563372 |
| 14 | 623.4 | 44.6 | 929 | 9 | AI226504 |
| 15 | 618 | 44.3 | 660 | 10 | AV661154 |
| 16 | 613.2 | 44.0 | 637 | 10 | AM963431 |
| 17 | 609.4 | 43.7 | 613 | 10 | AV647573 |
| 18 | 605.4 | 43.4 | 647 | 10 | AV690599 |
| 19 | 605.2 | 43.4 | 825 | 13 | BI219765 |
| 20 | 596.2 | 42.7 | 813 | 13 | BI218192 |
| 21 | 586.8 | 42.1 | 824 | 13 | BI148282 |
| 22 | 583.8 | 41.8 | 775 | 12 | BG567126 |
| 23 | 583.6 | 41.8 | 660 | 10 | AV691885 |
| 24 | 580.4 | 41.6 | 806 | 13 | BI148093 |
| 25 | 579 | 41.5 | 621 | 9 | AA706894 |
| 26 | 579 | 41.5 | 647 | 12 | BG562782 |
| 27 | 577.6 | 41.4 | 935 | 12 | BP533531 |
| 28 | 576.4 | 41.3 | 980 | 13 | BI147005 |
| 29 | 576 | 41.3 | 645 | 10 | AV682911 |
| 30 | 573 | 41.1 | 880 | 13 | BI331277 |
| 31 | 572.2 | 41.1 | 871 | 13 | BI328537 |
| 32 | 567.6 | 40.7 | 858 | 13 | BI148112 |
| 33 | 564.2 | 40.4 | 623 | 10 | AV661792 |
| 34 | 563.2 | 40.4 | 805 | 9 | AI048646 |
| 35 | 563 | 40.4 | 805 | 13 | BI246571 |
| 36 | 559.6 | 40.1 | 867 | 13 | BI218917 |
| 37 | 559 | 40.1 | 727 | 9 | AI419883 |
| 38 | 557.2 | 39.9 | 659 | 10 | AV690770 |
| 39 | 557 | 39.9 | 858 | 13 | BI328265 |
| 40 | 554.8 | 39.8 | 845 | 9 | AI530232 |
| 41 | 554 | 39.7 | 626 | 10 | AV653330 |
| 42 | 552.8 | 39.6 | 845 | 13 | BI219596 |
| 43 | 552.2 | 39.6 | 771 | 12 | BG617043 |
| 44 | 551.6 | 39.5 | 626 | 10 | AM963364 |
| 45 | 551.6 | 39.5 | 872 | 13 | BI328534 |

ALIGNMENTS

RESULT 1
LOCUS AF130100 1794 bp mRNA linear HTC 08-MAY-2001
DEFINITION Homo sapiens clone FLB1413 PRO0309 complete cds.
ACCESSION AF130100
VERSION AF130100.1 GI:11493503
KEYWORDS
SOURCE
ORGANISM Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (bases 1 to 1794)
Zhang, C., Yu, Y., Zhang, S., Wei, H., Bi, J., Zhou, G., Dong, C., Zai, Y., Xu, W., Gao, F., Liu, M. and He, F.
Functional prediction of the coding sequences of 75 new genes deduced by analysis of cDNA clones from human fetal liver
Unpublished
JOURNAL
REFERENCE
2 (bases 1 to 1794)
Zhang, C., Yu, Y., Zhang, S., Wei, H., Bi, J., Zhou, G., Dong, C., Zai, Y., Xu, W., Gao, F., Liu, M. and He, F.
Direct Submission
Submitted (23-FEB-1999) Department of Experimental Hematology,
Institute of Radiation Medicine, Beijing Taping Road 27, Beijing,
Beijing 100850, P. R. China
JOURNAL
AUTHORS
FEATURES
SOURCE
1. 1794
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="FLB1413"

REFERENCE 1 (bases 1 to 831)
 AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
 TITLE Full-length cDNA libraries and normalization
 JOURNAL Unpublished (2001)
 COMMENT Contact: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 EVRY cedex - France
 Email: segre@genoscope.cns.fr, Web : www.genoscope.cns.fr.
 Location/Qualifiers
 1. 831
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 /clone_1ib="LTI_NFL001_NBC4"
 /sex="male"
 /tissue_type="neuroblastoma cells"
 /lab_host="DH10B"
 /note="Organ: Brain; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact: Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : filiang@lifetech.com URL : http://fulllength.invitrogen.com"

BASE COUNT 226 a 224 c 186 g 194 t 1 others

ORIGIN

Query Match 53.2%; Score 742.2; DB 9; Length 831;
 Best Local Similarity 99.3%; Pred. No. 5.2e-200;
 Matches 744; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

1 ATGTATTCAGATGTAGAGAACTGTAACCTCGAGAAAGAGGTTATCTTTGTC 60
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 83 ATGTATTCAGATGTAGAGAACTGTAACCTCGAGAAAGAGGTTATCTTTGTC 142
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 61 TTGCTGCTCATTTGGCTTTGGAAGCTGAGACCTGTCACGGAGCCCTGTGACATCTGC 120
 |||
 143 TTGCTGCTCATTTGGCTTTGGAAGCTGAGACCTGTCACGGAGCCCTGTGACATCTGC 202
 |||
 121 ACAGCCAAAGCGCGGACATTTCCATGATCCCATGTCATTTACCGCTCCCGGAGAA 180
 |||
 203 ACAGCCAAAGCGCGGACATTTCCATGATCCCATGTCATTTACCGCTCCCGGAGAA 262
 |||
 181 AAGGCAACTGAGATGAGGCTCAGAACAGAAATCCCGAGGCCCAACCGGCGTGC 240
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 263 AAGGCAACTGAGATGAGGCTCAGAACAGAAATCCCGAGGCCCAACCGGCGTGC 322
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 241 TGGGAACGTGTCAGAGCCATTCGCTTTGTCACACTTTCTATGACACCTGACAGAT 300
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 323 TGGGAACGTGTCAGAGCCATTCGCTTTGTCACACTTTCTATGACACCTGACAGAT 382
 |||
 301 TCCAGAAATGACATGATTAACATTTCTGTCACCCCTGAGTATCTCCAGGCTTTGCT 360
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 383 TCCAGAAATGACATGATTAACATTTCTGTCACCCCTGAGTATCTCCAGGCTTTGCT 442
 |||
 361 ATGACCAAGCTGGTGCTGTATGACACCTCCAGCAATGATGAGGATTTAAGTT 420
 |||
 443 ATGACCAAGCTGGTGCTGTATGACACCTCCAGCAATGATGAGGATTTAAGTT 502
 |||
 421 GACACCATATCTGAGAAACATCTGATCAGATCACTTTCTTTGCAAACTGAACTGC 480
 |||
 503 GACACCATATCTGAGAAACATCTGATCAGATCACTTTCTTTGCAAACTGAACTGC 562
 |||
 481 CGACTATGAGAAAGCAAAATCTCTCAAGTGTATGACCAATGCTGCTTTTGA 540
 |||
 563 CGACTATGAGAAAGCAAAATCTCTCAAGTGTATGACCAATGCTGCTTTTGA 622
 |||
 541 GACAAATCCCTTCAATGAGACCTACCAAGACATGAGTGTATGAGGC 600
 |||
 623 GACAAATCCCTTCAATGAGACCTACCAAGACATGAGTGTATGAGGC 682

601 AAGCTCCAGCCCTTGACTTCAAGGAAATGACAGCATTCAGAGCGGCATCAACAA 660
 683 AAGCTCCAGCCCTTGACTTCAAGGAAATGACAGCATTCAGAGCGGCATCAACAA 742
 661 TGGGTGCTCAATTAAGCCGAAAGCCGATCAACCATTCCTCGGAGCCATCAT 720
 743 TGGGTGCTCAATTAAGCCGAAAGCCGATCAACCATTCCTCGGAGCCATCAT 802
 721 GAGTCACATGTTCTGCTGCTGTTAACAC 749
 803 GAGTCACATGTTCTGCTGCTGTTAACAC 831

RESULT 4
 AL564291/c 826 bp mRNA linear EST 16-FEB-2001
 LOCUS AL564291 LTI_NFL001_NBC4 Homo sapiens cDNA clone CSODM004YG18 3
 DEFINITION prime, mRNA sequence.
 ACCESSION AL564291
 VERSION AL564291.1 GI:12914549
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 826)
 AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
 TITLE Full-length cDNA libraries and normalization
 JOURNAL Unpublished (2001)
 COMMENT Contact: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 EVRY cedex - France
 Email: segre@genoscope.cns.fr, Web : www.genoscope.cns.fr.
 Location/Qualifiers
 1. 826
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_lib="CSODM004YG18"
 /clone_1ib="LTI_NFL001_NBC4"
 /sex="male"
 /tissue_type="neuroblastoma cells"
 /lab_host="DH10B"
 /note="Organ: Brain; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact: Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : filiang@lifetech.com URL : http://fulllength.invitrogen.com"

BASE COUNT 177 a 189 c 220 g 198 t 42 others

ORIGIN

Query Match 52.6%; Score 733.6; DB 9; Length 826;
 Best Local Similarity 90.4%; Pred. No. 1.5e-197;
 Matches 746; Conservative 35; Mismatches 43; Indels 1; Gaps 1;

570 CCAGACATCATGAGTGTATGAGCCAGCTCCAGCCCTGAGCTTCAAGGAAA 629
 |||
 825 CCAGACATCATGAGTGTATGAGCCAGCTCCAGCCCTGAGCTTCAAGGAAA 766
 |||
 630 TCCAGAGCATCAAGCGGCGCATCAACAAATGGGTGTCATTAAGCCGAGCGAAT 689
 |||
 765 TCCAGAGCATCAAGCGGCGCATCAACAAATGGGTGTCATTAAGCCGAGCGAAT 706
 |||
 690 CACGATGATCTTCTTGGAAAGCATCATGAGCTCACTGTTGCTGCTGTTAAC 749
 |||
 705 CACGATGATCTTCTTGGAAAGCATCATGAGCTCACTGTTGCTGCTGTTAAC 646
 |||
 750 CATTATCTCAAGGCGCTGTGAAGTCAAGTTCAGCCCTGAGAACACAGAGGAAT 809

| LOCUS | AI207425 | 666 bp | mRNA | linear | EST 11-NOV-1993 |
|-----------------------|--|-------------|------|--------|-----------------|
| DEFINITION | HA2767 Human fetal liver cDNA library Homo sapiens cDNA, mRNA | | | | |
| ACCESSION | AI207425 | | | | |
| VERSION | AI207425.1 | GI:65161433 | | | |
| KEYWORDS | EST. | | | | |
| SOURCE | human. | | | | |
| ORGANISM | Homo sapiens | | | | |
| REFERENCE | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo. | | | | |
| AUTHORS | Yu, Y., Zhang, C., Luo, L., Ouyang, S., Li, W., Wu, J., Zhou, S., Liu, M., and He, F. | | | | |
| TITLE | Expression profile analysis of a human fetal liver cDNA library | | | | |
| JOURNAL | Unpublished (1999) | | | | |
| COMMENT | Contact: Chengang Zhang
Beijing Institute of Radiation Medicine
27 Taiding Road, Beijing 100850, P.R.China
Email: zhang_chengang@hotmail.com. | | | | |
| FEATURES | Location/Qualifiers | | | | |
| source | 1..666 | | | | |
| | /organism="Homo sapiens" | | | | |
| | /db_xref="taxon:9606" | | | | |
| | /clone_lib="Human Fetal liver cDNA library" | | | | |
| | /tissue_type="liver" | | | | |
| | /dev_stage="fetal" | | | | |
| | /lab_host="MC1061/P3" | | | | |
| | /note="Vector: pCDNA1" | | | | |
| BASE COUNT | 171 a 161 c 186 g 148 t | | | | |
| ORIGIN | | | | | |
| Query Match | 47.7%; Score 666; DB 9; Length 666; | | | | |
| Best Local Similarity | 100.0%; Pred. No. 2,36-178; | | | | |
| Matches | 666; Conservative 0; Mismatches 0; Indels 0; Gaps 0; | | | | |
| OY | 647 CGGCCATACAAAGGGGTGTCATTAGACCGGAGGCGCAATCCGATGTCATTCCCT | 706 | | | |
| DB | 1 CGGCCATACAAAGGGGTGTCATTAGACCGGAGGCGCAATCCGATGTCATTCCCT | 60 | | | |
| OY | 707 CGGAAGCATCATAGTCACTGTTCTGTGTCGTGTTAACACATTACTTCAAGGACC | 766 | | | |
| DB | 61 CGGAAGCATCATAGTCACTGTTCTGTGTCGTGTTAACACATTACTTCAAGGACC | 120 | | | |
| OY | 767 TGTGAAGTCAAGTTCAGCCTTGGAACAAGAGAACTGTTTCAAGCTATG | 826 | | | |
| DB | 121 TGTGAAGTCAAGTTCAGCCTTGGAACAAGAGAACTGTTTCAAGCTATG | 180 | | | |
| OY | 827 GAGAGTCGTGTCACATCTATGATGTACACAGAGGCAAGTTCGTTATGGCGCGTGG | 886 | | | |
| DB | 181 GAGAGTCGTGTCACATCTATGATGTACACAGAGGCAAGTTCGTTATGGCGCGTGG | 240 | | | |
| OY | 887 CTGAAGGCAACCGAGTGTGAGTTGCCCTTCAAGGTGATGATCAATCATGTGCTCA | 946 | | | |
| DB | 241 CTGAAGGCAACCGAGTGTGAGTTGCCCTTCAAGGTGATGATCAATCATGTGCTCA | 300 | | | |
| OY | 947 TCTTGCCCAAGCTGAGAGAGCGCTGGCCAGAGTGAAGAACTCAACCCAGAGTGC | 1006 | | | |
| DB | 301 TCTTGCCCAAGCTGAGAGAGCGCTGGCCAGAGTGAAGAACTCAACCCAGAGTGC | 360 | | | |
| OY | 1007 TGCAGAGTGGCTGATGATTTGAGAGAGATGATCGTGTGTCACATGCCGCTTCC | 1066 | | | |
| DB | 361 TGCAGAGTGGCTGATGATTTGAGAGAGATGATCGTGTGTCACATGCCGCTTCC | 420 | | | |
| OY | 1067 GCATTGAGAGCGGCTTCAATTGAGAGAGACAGTCAAGACATGGGCTTGTGATCTGT | 1126 | | | |
| DB | 421 GCATTGAGAGCGGCTTCAATTGAGAGAGACAGTCAAGACATGGGCTTGTGATCTGT | 480 | | | |
| OY | 1127 TCAGCGCTGAAGAGTCCAAAGCTCCAGAGTATTTGGCAAGAGCGCGAGTACCTCTATG | 1186 | | | |
| DB | 481 TCAGCGCTGAAGAGTCCAAAGCTCCAGAGTATTTGGCAAGAGCGCGAGTACCTCTATG | 540 | | | |
| OY | 1187 TCTCAGATGATTCATTAAGGCAATTTCTTGAAGTAATGAAGAGGCAAGTGAAGCACTG | 1246 | | | |

| | | | |
|-----------------------|------|---|-----------------------------|
| Db | 541 | TCTCAGATGCAITTCATAAAGGCATTCTTGTGGTAATAATGAAGAAGCGACGTAAACAGCTG | 600 |
| OY | 1247 | CAACTACCCTGTTTGATATGTCGCGCGTTCCGTAACCCCAACAAGGCTGACTTTCAAG | 1306 |
| Db | 601 | CAATTAACCGCTGTGTATGTCGTGCGCGTTCCGTAACCCCAACAAGGCTGACTTTCAAG | 660 |
| OY | 1307 | CCAACA 1312
 | |
| Db | 661 | CCAACA 666 | |
| RESULT 7 | | | |
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| LOCUS | | | |
| DEFINITION | | 602586477F1 NIH_MGC_76 Homo sapiens cDNA clone IMAGE:4715251 5' | |
| ACCESSION | | | |
| KEYWORDS | | | |
| SOURCE | | | |
| ORGANISM | | | |
| REFERENCE | | | |
| AUTHORS | | | |
| TITLE | | | |
| JOURNAL | | | |
| COMMENT | | | |
| FEATURES | | | |
| source | | | |
| BASE COUNT | | | |
| ORIGIN | | | |
| Query Match | | | |
| Best local similarity | | | |
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| OY | 1 | ATGATATTCATATGATAGTAGAACCTGTACCTCTGGAAAAAGGAAGGTTATCTTTTGGC | 60 |
| Db | 70 | ATGATATTCATATGATAGTAGAACCTGTACCTCTGGAAAAAGGAAGGTTATCTTTTGGC | 129 |
| OY | 61 | TTGCTGCTCATATGCTTCTGGAGCTGCGTGAACCTGTCAACGGAGCCCTGTGACATCTGC | 120 |
| Db | 130 | TTGCTGCTCATATGCTTCTGGAGCTGCGTGAACCTGTCAACGGAGCCCTGTGACATCTGC | 189 |
| OY | 121 | ACAGCCAAAGCGCGGGGACATTTCCATATGCCATATGTCATTTTACCGCTCCCGGAGAG | 180 |
| Db | 190 | ACAGCCAAAGCGCGGGGACATTTCCATATGCCATATGTCATTTTACCGCTCCCGGAGAG | 249 |

181 AAGCACTGAGATGATGAGCTCAGAGAGAGATCCGGAGGCCACCAACCGGCGTTC 240
 Db AAGGCACTGAGATGAGAGGCTCAGAGAGAGATCCGGAGGCCACCAACCGGCGTTC 309
 Qy 241 TGGGAGCTGTCAGAGGCAATTCGGCTTGTGCTACCACTTTCTATCAGACCTGACAGAT 300
 Db 310 TGGGAGCTGTCAGAGGCAATTCGGCTTGTGCTACCACTTTCTATCAGACCTGACAGAT 369
 Qy 301 TCCAGAGATGACATGATACATTTTCTGTGATACCCCTGAGATATCTCCAGCGCTTTGCT 360
 Db 370 TCCAGAGATGACATGATACATTTTCTGTGATACCCCTGAGATATCTCCAGCGCTTTGCT 429
 Qy 361 ATGACCAAGCTGGGAGCTGTATAGACACCTTCAGCACTGATGAGGATTTTAAGTTT 420
 Db 430 ATGACCAAGCTGGGAGCTGTATAGACACCTTCAGCACTGATGAGGATTTTAAGTTT 489
 Qy 421 GACACCATATCTGAGAGAAACATCTGATGATGATCACTTTCTTTGCCAACTGAACTGC 480
 Db 490 GACACCATATCTGAGAGAAACATCTGATGATGATCACTTTCTTTGCCAACTGAACTGC 549
 Qy 481 GCACTCTATCCAGAAAGCCCAAAATCTCCAAATTAGTATCAGCCCAATCGCTTTTGGGA 540
 Db 550 GCACTCTATCCAGAAAGCCCAAAATCTCCAAATTAGTATCAGCCCAATCGCTTTTGGGA 609
 Qy 541 GACAAATCCCTTACCTTCAATGAGACCTACAGAGCATCAGATGATGATGATGAGGCC 600
 Db 610 GACAAATCCCTTACCTTCAATGAGACCTACAGAGCATCAGATGATGATGATGAGGCC 669
 Qy 601 AAGCTCCAGCCCTT-GAGACTTCAGAGAAA--TGACAGAGCATCAGAGCGGCATCAACA 658
 Db 670 AAGCTCCAGCCCTTGGAGCTTCAAGAGAAATCGAGAGCAATCGAGCGGCATCAACA 729
 Qy 659 AATGGGTCTCCAAATAG-ACCGAAGCGGATCACCAGATGTATTC 704
 Db 730 AATGGGTCTCCAAATAG-ACCGAAGCGGATCACCAGATGTATTC 776

RESULT 8
 AV653910 725 bp mRNA linear EST 15-JAN-2002
 LOCUS AV653910 GLC Homo sapiens cDNA clone GLCDPH09 3', mRNA sequence.
 DEFINITION AV653910
 ACCESSION AV653910.1 GI:9874924
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE
 AUTHORS
 Xu X., Huang J., Xu Z., Qian B., Zhu Z., Yan Q., Cai T., Zhang X.,
 Xiao H., Qu J., Liu F., Huang Q., Cheng Z., Li N., Du J., Hu W.,
 Shen K., Lu G., Fu G., Zhong M., Xu S., Gu W., Huang W., Zhao X.,
 Hu G., Gu J., Chen Z., and Han Z.
 Insight into hepatocellular carcinogenesis at transcriptome level
 by comparing gene expression profiles of hepatocellular carcinoma
 with those of corresponding noncancerous liver
 Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)
 21625106
 JOURNAL
 MEDLINE
 COMMENT
 Contact: Zeguang Han
 Chinese National Human Genome Center at Shanghai
 351 Guoshoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
 201203, P. R. China
 Tel: 86-21-50801919 (ex. 45)
 Fax: 86-21-50801922
 Email: hanzg@chgc.sh.cn
 This clone is available at CHGC in Shanghai.

FEATURES

source
 1..725
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="GLCDPH09"
 /clone_1ib="GLC"

/tissue type="corresponding non cancerous liver tissue"
 /dev stage="Adult"
 /lab_host="SOLR"
 /note=Vector: Bluescript sk(-), Site_1: EcoRI; Site_2:
 XhoI

Query Match 46.9%; Score 653.8; DB 10; Length 725;
 Best Local Similarity 98.6%; Pred. No. 7.4e-175;
 Matches 680; Conservative 0; Mismatches 8; Indels 2; Gaps 2;

BASE COUNT 195 a 177 c 191 g 160 t 2 others
 ORIGIN
 Qy 459 CTTCTTGGCCAACTGAACTGCGAGCTCTATCGAAAAGCCAAACAAATCTCCAAATTAGT 518
 Db 1 CTTCTTGGCCAACTGAACTGCGAGCTCTATCGAAAAGCCAAACAAATCTCCAAATTAGT 60
 Qy 519 ATCAGCCAAATGCGCTTTTGGAGACAAATCCCTTACCTTCAATGAGACTTACAGAGAT 578
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 Qy 579 CAGTGAATGATATGAGAGCCCAAGCTTCAGCCCTTGAATCTTCAAGAAAATGAGAGCA 638
 Db 121 CAGTGAATGATATGAGAGCCCAAGCTTCAGCCCTTGAATCTTCAAGAAAATGAGAGCA 180
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 Db 181 ATCCAGAGCGGCGCATCAACAAATGGGTGTCATTAAGACGAGAGCGGCAATCACCGATGT 240
 Qy 699 CATTCCCTCGGAGACCATCAATGAGCTCACTGTTCTGGTGTGTTAACACCATTTACTT 758
 Db 241 CATTCCCTCGGAGACCATCAATGAGCTCACTGTTCTGGTGTGTTAACACCATTTACTT 300
 Qy 759 CAAGGCGCTGTGGAAGTCAAAAGTTCAAGCTTGAAGAACAGAGAAAGTCTTCAAA 818
 Db 301 CAAGGCGCTGTGGAAGTCAAAAGTTCAAGCTTGAAGAACAGAGAAAGTCTTCAAA 360
 Qy 819 GAGTGAATGAGAGTGTGTTGATGATGATGATGATGATGATGATGATGATGATGATGATG 878
 Db 361 GAGTGAATGAGAGTGTGTTGATGATGATGATGATGATGATGATGATGATGATGATGATG 420
 Qy 879 GCGGCTGCTGAGAGAGCCAGAGCTGTTGAGTTGCCCTTCAAGAGTGAATGATGATGATG 938
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 Qy 939 GGTCTCTATCTTCCCAAGCTTGAAGAGAGCTTGGCCCAAGGTGAGAGAACTTCAACCC 998
 Db 481 GGTCTCTATCTTCCCAAGCTTGAAGAGAGCTTGGCCCAAGGTGAGAGAACTTCAACCC 540
 Qy 999 AGAGGTGCTGAGAGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1057
 Db 541 AGAGGTGCTGAGAGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 600
 Qy 1058 CCCGCTTCCGATGAGAGAGCGCTTCAAGTTGAAGAGAGAGAGAGAGAGAGAGAGAGAG 1116
 Db 601 CCCGCTTCCGATGAGAGAGCGCTTCAAGTTGAAGAGAGAGAGAGAGAGAGAGAGAGAG 660
 Qy 1117 GTCGATCTGTTCAAGCCCTGAAAAGTCCAA 1146
 Db 661 GTCGATCTGTTCAAGCCCTGAAAAGTCCAA 690

RESULT 9
 A1255692 905 bp mRNA linear EST 12-NOV-1998
 LOCUS A1255692
 DEFINITION u156e10.y1 Sugano mouse liver m1a Mus musculus cDNA clone
 IMAGE:1886442 5' similar to gb:568793_rnal ANTIYTHROMBIN-III
 PRECURSOR (HUMAN);, mRNA sequence.
 ACCESSION A1255692
 VERSION A1255692.1 GI:3863217
 KEYWORDS
 SOURCE
 ORGANISM
 EST.
 house mouse.
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;


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/clone="IMAGE:5051423"
/lab_host="NCI CGAP L19"
/Note="Organ: liver; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.9 kb. Constructed by Life
Technologies. Note: this is a NCI CGAP library."
BASE COUNT      230 a      227 c      232 g      193 t
ORIGIN

```

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Query Match      46.3%; Score 646; DB 13; Length 882;
Best Local Similarity 86.2%; Pred. No. 1.4e-172;
Matches 726; Conservative 0; Mismatches 115; Indels 1; Gaps 1;

543 CAAATCCCTTACCTTCAATGAGACCTACAGACATCATGATGTTGATATGAGCCAA 602
1 CAAATCCCTTACCTTCAATGAGACCTATCAATATGTTGATGAGTTGTTATGAGCCAA 60
603 GCTCCAGCCCTGAGCTTCAAGAGAAATGCAAGAGATCCAGAGCGCCATCAAGATG 662
61 GCTCCAGCCCTGAGCTTCAAGAGAAATCCGAGAGATCCAGAGTACCATTAACACTG 120
663 GGTGTCATTAAGACCGAGGCGGATCCGATCATTCCTCGGAAAGCCATCAATGA 722
121 GGTAGCTAATAAGACTGAAGGCGGATCAAGATGTATCCACAGGCGGCATTAACGA 180
723 GGTCACTGTTGCTGCTGTTAACAACATTTACTTCAAGGCGCTGTGGAAGTCAAGTT 782
181 GGTCACTGCTGCTGCTGTTAACAACATTTACTTCAAGGCGCTGTGGAAGTCAAGTT 240
783 CAGCCCTGAGAACAGAGAGAGAGACTGTTTCAAGGCGTGTGAGAGATCGTTTCAGC 842
241 CAGCCCTGAGAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300
843 ATCTATGATGATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 902
301 GCTTATGATGATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
903 GCTTATGATGATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 962
361 GCTTATGATGATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
963 GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1022
421 GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
1023 TGAATTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1082
481 TGAGCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
1083 CAGTTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1142
541 CAGTTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 600
1143 CAAATCCCTTACCTTCAATGAGACCTACAGACATCATGATGTTGATGAGCCAA 1202
601 CCAATCCCTTACCTTCAATGAGACCTACAGACATCATGATGTTGATGAGCCAA 660
1203 TAAAGCAATTTCTTGAAGTAAATGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1262
661 CAAACCAATTTCTTGAAGTAAATGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
1263 GATTCCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1322
721 GATTCCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 780
1323 GATTCCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1381
781 GATTCCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 840
1382 CT 1383
841 TT 842

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```

RESULT 11
BS656905      852 bp      mRNA      linear      EST 10-APR-2001
LOCUS         602588332F1 NIH_MGC_76 Homo sapiens CDNA clone IMAGE:4722655 5',
DEFINITION    mRNA sequence.
ACCESSION     BS656905
VERSION       BS656905.1 GI:13576748
KEYWORDS      EST.
SOURCE         human.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

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REFERENCE     1 (bases 1 to 852)
AUTHORS       NIH-MGC http://mgs.nci.nih.gov/.
TITLE         National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL       Unpublished (1999)
COMMENT       Contact: Robert Strausberg, Ph.D.
              Email: sgabbs@email.nih.gov
              Tissue Procurement: CLONTECH Laboratories, Inc.
              CDNA Library Preparation: CLONTECH Laboratories, Inc.
              DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
              DNA Sequencing by: Incyte Genomics, Inc.
              Clone distribution: MGC clone distribution information can be
              found through the I.M.A.G.E. Consortium/LNL at:
              http://image.lnl.gov
              Plate: LNCMI580 row: 0 column: 08
              High quality sequence stop: 769.

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FEATURES

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1..852
location/Qualifiers
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    /db_xref="taxon:9606"
    /clone="IMAGE:4722655"
    /lab_host="NIH_MGC_76"
    /note="Organ: liver; Vector: pDNR-LIB (Clontech); Site 1:
    SfiI (ggcgccctggcc); Site 2: SfiI (ggcgccctggcc); 5' and
    3' adaptors were used in cloning as follows: 5' adaptor
    sequence: 5'-CACGCCATTAATGCG-3' and 3' adaptor sequence:
    5'-ATCTAGAGCGGAGGCGCGGAGATG-3' (30)BN-3' (where B = A,
    C, or G and N = A, C, G, or T). Average insert size 1.85
    kb (range 1.0-4.0 kb). 15/15 colonies contained inserts
    by PCR. This library was enriched for full-length clones
    and was constructed by Clontech Laboratories (Palo Alto,
    CA). Note: this is a NIH_MGC Library."

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BASE COUNT

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230 a      232 c      197 g      193 t
ORIGIN

```

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Query Match      45.5%; Score 635.2; DB 12; Length 852;
Best Local Similarity 95.0%; Pred. No. 1.7e-169;
Matches 754; Conservative 0; Mismatches 28; Indels 12; Gaps 9;

1 ATGATTTCCATGATGATGAGAACTGTAACTCTGAGAAAGAGTTATCTTTTGTCC 60
49 ATGATTTCCATGATGATGAGAACTGTAACTCTGAGAAAGAGTTATCTTTTGTCC 108
61 TTGCTGCTCAATGCTTCTGAGAGCTGCTGAGCTGTCAAGGAGCCCTGTGGAATTCG 120
109 TTGCTGCTCAATGCTTCTGAGAGCTGCTGAGCTGTCAAGGAGCCCTGTGGAATTCG 168
121 AAGGCAAGCGCGGAGATTCATCCATGAATCCCATGTCATTTACCGCTCCCGGAGAG 180
169 AAGGCAAGCGCGGAGATTCATCCATGAATCCCATGTCATTTACCGCTCCCGGAGAG 228
181 AAGGCAAGCGCGGAGATTCATCCATGAATCCCATGTCATTTACCGCTCCCGGAGAG 240
229 AAGGCAAGCGCGGAGATTCATCCATGAATCCCATGTCATTTACCGCTCCCGGAGAG 288
241 TGGGAAGCTGTCAAGGCAATTCCTGCTTGTCTACCACTTTCTATCAGCACTGCGAGAT 300
289 TGGGAAGCTGTCAAGGCAATTCCTGCTTGTCTACCACTTTCTATCAGCACTGCGAGAT 348

```

QY 301 TCACAAATGACATATTAACATTTTCTGTCAACCCCTGAGTATCTCCAGGCTTTTGTCT 360
 DB 349 TCCAAATAATGACATATTAACATTTTCTGTCAACCCCTGAGTATCTCCAGGCTTTTGTCT 408
 QY 361 ATGACCAAGCTGGGCTGTATGACACCCCTCAGCA--CTGATGAGGATTTTAAGTT 419
 DB 409 ATACCAAGCTGGGCTGTATGACACCCCTCAGCAACCTGATGAGGATTTTAAGTT 468
 QY 420 TGAACCATATCTGAGAAAAACATCTGATGATGATCACTTCTTTGCCAACTGAATG 479
 DB 469 TGAACCATATCTGAGAAAAACATCTGATGATGATCACTTCTTTGCCAACTGAATG 528
 QY 480 CCGACTCTATCGAAAGCCCAACAATCTTC--AAGTTAGTATGAGCAATCGCTTTTGG 538
 DB 529 CCGACTCTATCGAAAGCCCAACAATCTTC--AAGTTAGTATGAGCAATCGCTTTTGG 588
 QY 539 GAGACAATATCCCTTACC--TTCAATGAGACCTACGAGACATGAGTGTATGAG 597
 DB 589 GAGACAATATCCCTTACC--TTCAATGAGACCTACGAGACATGAGTGTATGAG 648
 QY 598 GCCAAGCTCCAGCCCTCTGACCTTCAA--GGAAATGACAGCAATCCAGAGCGGCATC 654
 DB 649 GCCAAGCTCCAGCCCTCTGACCTTCAA--GGAAATGACAGCAATCCAGAGCGGCATC 708
 QY 655 AACAAATGGGTCTTCAATAAGA--CCGAGGCCGATCAGCATGATCTTCCCTCGAAGC 713
 DB 709 AACAAATGGGTCTTCAATAAGA--CCGAGGCCGATCAGCATGATCTTCCCTCGAAGC 768
 QY 714 CATCAATGAGCTACTGTTCTGTGCTGTATTAACACATTTACTTCAAGGCGCTGTGAA 773
 DB 769 CATC-ATGAGCTACTG-TCGTGTCTGAT-ACACCGAGTACTTCAAG--CTCGGAA 823
 QY 774 GTCAAGTTGAGCC 787
 DB 824 GTCAAGTTGAGCC 837

RESULT 12
 LOCUS AV682065 675 bp mRNA linear EST 16-JUN-2002
 DEFINITION AV682065 GRX Homo sapiens cDNA clone GKBAB07 5', mRNA sequence.
 ACCESSION AV682065
 VERSION AV682065.1 GI:10283928
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 1 (bases 1 to 675)
 Xu, X., Huang, J., Xu, Z., Qian, B., Zhu, Z., Yan, Q., Cai, T., Zhang, X.,
 Xiao, H., Qu, J., Liu, F., Huang, Q., Cheng, Z., Li, N., Du, J., Hu, W.,
 Shen, K., Lu, G., Fu, G., Zhong, M., Xu, S., Gu, W., Huang, W., Zhao, X.,
 Hu, G., Gu, Z., Chen, Z. and Han, Z.
 Insight into hepatocellular carcinogenesis at transcriptome level
 by comparing gene expression profiles of hepatocellular carcinoma
 with those of corresponding noncancerous liver
 Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)
 21625106
 COMMENT Contact: Zeguang Han
 Chinese National Human Genome Center at Shanghai
 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
 201203, P. R. China
 Tel: 86-21-50801919 (ex.45)
 Fax: 86-21-50801922
 Email: hanzg@chgc.sh.cn
 This clone is available at CHGC in Shanghai.
 Location/Qualifiers
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 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="GKBAB07"
 /clone_1ib="GKB"
 /tissue_type="hepatocellular carcinoma"

FEATURES
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/dev_stage="Adult"
 /lab_host="SOLR"
 /note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
 XhoI"
 BASE COUNT 180 a 167 c 177 g 147 t 4 others

Query Match 45.5%; Score 634.6; DB 10; Length 675;
 Best Local Similarity 97.8%; Pred. No. 2.1e-169;
 Matches 662; Conservative 0; Mismatches 13; Indels 2; Gaps 2;

QY 459 CTTCTTGGCAACGAACTGCGCACTGATGAAAGCAACAATCCTCAAGTTAGT 518
 DB 1 CTTCTTGGCAACGAACTGCGCACTGATGAAAGCAACAATCCTCAAGTTAGT 60
 QY 519 ATACGCAATCGCCTTTTGGAGCAAAATCCCTTCAATGAGACTTACAGACAT 578
 DB 61 ATACGCAATCGCCTTTTGGAGCAAAATCCCTTCAATGAGACTTACAGACAT 120
 QY 579 CAGTGAATTGTATATGAGCCAGCTCCAGCCCTGACCTTCAAGAAATGACAGCA 638
 DB 121 CAGTGAATTGTATATGAGCCAGCTCCAGCCCTGACCTTCAAGAAATGACAGCA 180
 QY 639 ATCCAGAGCGGCATCAACAATGGGTGTCCAAATAAGCCGAAGCCGATCAGCAT 698
 DB 181 ATCCAGAGCGGCATCAACAATGGGTGTCCAAATAAGCCGAAGCCGATCAGCAT 740
 QY 699 CATTCCTCGAAGCATCAATGAGCTCACTGTTCTGTGTCTGTTAAACCATTTACT 758
 DB 241 CATTCCTCGAAGCATCAATGAGCTCACTGTTCTGTGTCTGTTAAACCATTTACT 300
 QY 759 CAAGGCGCTGTGAAAGTCAAAGTTCAAGCTTGAACACAGAAAGAACTGTTCAAA 818
 DB 301 CAAGGCGCTGTGAAAGTCAAAGTTCAAGCTTGAACACAGAAAGAACTGTTCAAA 860
 QY 819 GGCTGATGAGAGTGTGTGTGATGATGATGATGATGATGATGATGATGATGATG 878
 DB 361 GGCTGATGAGAGTGTGTGTGATGATGATGATGATGATGATGATGATGATGATG 420
 QY 879 GCGCGTGTGTAAGGACCCAGAGTCTTGAAGTTCCTTCAAGGTGATGATGATGAT 938
 DB 421 GCGCGTGTGTAAGGACCCAGAGTCTTGAAGTTCCTTCAAGGTGATGATGATGAT 480
 QY 939 GGTCTCATCTTGGCCCAAGCTTGAAGAGAGCTTGGCCCAAGGTGAGAGAGAGAG 998
 DB 481 GGTCTCATCTTGGCCCAAGCTTGAAGAGAGAGCTTGGCCCAAGGTGAGAGAGAG 540
 QY 999 AAGAGGTGTCAGAGAGTGGCTGATGAATGAGAGAGATGATGATGATGATGATG 1058
 DB 541 AAGAGGTGTCAGAGAGTGGCTGATGAATGAGAGAGATGATGATGATGATGATG 600
 QY 1059 CCGCTTCCGATTTGAGAGAGCGGCTTGAAGTTGAGAGAGAGAGAGAGAGAGAG 1118
 DB 601 CCG-TTTCCGATTTGAGAGAGCGGCTTGAAGTTGAGAGAGAGAGAGAGAGAGAG 658
 QY 1119 CGATCTGTTCAGCCCTG 1135
 DB 659 CGATCTGTTCAGCCCTG 675

RESULT 13
 LOCUS BG563372 744 bp mRNA linear EST 10-APR-2001
 DEFINITION BG563372 602582428P1 NIH_MGC_76 Homo sapiens cDNA clone IMAGE:4710199 5',
 mRNA sequence.
 ACCESSION BG563372
 VERSION BG563372.1 GI:13571024
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 1 (bases 1 to 744)

AUTHORS NIH-MGC <http://mgi.nci.nih.gov/>;
National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov

Tissue Procurement: CLONETECH Laboratories, Inc.
cDNA Library Preparation: CLONETECH Laboratories, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
Plate: L1CM1548 row: h column: 08
High quality sequence stop: 739.
Location/Qualifiers

FEATURES

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/clone="IMAGE:4710199"
/clone_lib="NIH MGC 76"
/lab_host="DH10B (TI phage-resistant)"
/note="Organ: liver; Vector: pDNR-LIB (Clontech); Site 1: SfiI (ggcgctcgcc); Site 2: SfiI (ggcattatggcc); 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGCCATATGAGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGCCGCGGCGGAGCAGT-dT(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.85 kb (range 1.0-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH MGC Library."
BASE COUNT 203 a 200 c 170 g 171 t
ORIGIN

Query Match 45.0%; Score 628.2; DB 12; Length 744;
Best Local Similarity 98.4%; Pred. No. 1.5e-167;
Matches 666; Conservative 0; Mismatches 8; Indels 3; Gaps 3;

1 ATGTTTCCAAATGATAGAACTGTAACCTCTGAAAAAGAAAGTTATCTTTTTC 60
68 ATGTAATCCAAATGATAGAACTGTAACCTCTGAAAAAGAAAGTTATCTTTTTC 127
61 TTGCTGCTCATTTGCTTCTGAGCTGCGTCAAGGAGCCCTTGAGCATCTGC 120
128 TTGCTGCTCATTTGCTTCTGAGCTGCGTCAAGGAGCCCTTGAGCATCTGC 187
121 ACAGCCAAAGCCGCGGAGCATTTCCATGATCCCATGTCATTTACCGCTCCCGGAGAAG 180
188 ACAGCCAAAGCCGCGGAGCATTTCCATGATCCCATGTCATTTACCGCTCCCGGAGAAG 247
181 AAGGCACTGAGATGAGGAGCTCAGAAAGAAATCCCGGAGCCCAACCGGCGTGC 240
248 AAGGCACTGAGATGAGGAGCTCAGAAAGAAATCCCGGAGCCCAACCGGCGTGC 307
241 TGGGAATGTCAGAAAGCAATTCGCGCTTGGTCAACATTTCTATCAGACCTGGCAGAT 300
308 TGGGAATGTCAGAAAGCAATTCGCGCTTGGTCAACATTTCTATCAGACCTGGCAGAT 367
301 TCCAAAGATGACAAATGATTAATTTCTT-GTACCCCTGAGTATCTCCAGCGCTTTTGC 359
368 TCCAAAGATGACAAATGATTAATTTCTT-GTACCCCTGAGTATCTCCAGCGCTTTTGC 427
360 TATGACCAAGCTGGGCTGCTGTAATGACACCTCCAGCACTGATGAGATTTTAAGTT 419
428 TATGACCAAGCTGGGCTGCTGTAATGACACCTCCAGCACTGATGAGATTTTAAGTT 487
420 TGACACCAATATGAGAAACATCTGATGATCACTCTTCTTGCAAACTGAACATG 479
488 TGACACCAATATGAGAAACATCTGATGATCACTCTTCTTGCAAACTGAACATG 547
480 CGGACTCTATGAGAAAGCCCAAAATCTCCAGTTAGTATGAGCCCAATGCGCTTTTGG 539
548 CGGACTCTATGAGAAAGCCCAAAATCTCCAGTTAGTATGAGCCCAATGCGCTTTTGG 607

QY 540 AGACAAATCCC-TTACCTTCAATGAGACCTACAGACATCATGATGATATATGAG 598
DB 608 AGACAAATCCC-TTACCTTCAATGAGACCTACAGACATCATGATGATATATGAG 667
QY 599 CCAAGCTTCAGCCCTCGGACTTC-AAGAAATATCAGAGCAATCCAGAGCGCCATCAAC 657
DB 668 CCAAGCTTCAGCCCTCGGACTTC-AAGAAATATCAGAGCAATCCAGAGCGCCATCAAC 727
QY 658 AATGGGTGTCCATTA 674
DB 728 AATGGGTGTCCATTA 744

RESULT 14

LOCUS A1226504 929 bp mRNA linear EST 29-OCT-1998
DEFINITION u07c09.y1 Sugano mouse liver m1a Mus musculus cDNA clone
IMAGE:1891216 5' similar to gb:K68793_rnal ANTIHROMBIN-111
PRECUSOR (HUMAN);, mRNA sequence.

ACCESSION A1226504.1 GI:3809557
VERSION A1226504.1
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus

REFERENCE Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
Marras, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Stepien, M., Tan, F., Underwood, K., Moore, B.,
Thelander, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
Waterston, R.

TITLE The WashU-HMNI Mouse EST Project
JOURNAL Unpublished (1996)
COMMENT Contact: Marra M/Mouse EST Project
WashU-HMNI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810

Email: mouseest@wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MG1:975540

Seq primer: custom primer used
High quality sequence stop: 436.
Location/Qualifiers

FEATURES

source 1..929

/organism="Mus musculus"
/strain="C57BL"
/db_xref="taxon:10090"
/clone="IMAGE:1891216"
/clone_lib="Sugano mouse liver m1a"
/sex="Female"
/dev_stage="adult"
/lab_host="DH10B"
/note="Organ: liver; Vector: pME18S-FL3; Site 1: DraIII (CACTGTGTG); Site 2: DraIII (CACCAATGTG); 1st strand cDNA was primed with an oligo(dT) primer (ATGTGGCTTTTCTTTTCTTTT); double-stranded cDNA was ligated to a DraIII adaptor (TTGTTGGCTTACTGG) and cloned into distinct DraIII sites of the pME18S-FL3 vector (5' site CACTGTGTG, 3' site CACCAATGTG). XhoI should be used to isolate the cDNA insert. Size selection was performed to exclude fragments <1.5kb. Library constructed by Dr. Sumio Sugano (University of Tokyo Institute of Medical Science). Custom primers for sequencing: 5' end primer CTCTGCTCTTAAAGCTGCG and 3' end primer CGACCTGACCTGAGCACA."
BASE COUNT 244 a 251 c 231 g 203 t
ORIGIN

Db 421 AGTTCCTGAGTTCCTTCCTCAAGGTGATGACATCACCATGCTCCTCATCTTGCCCAAGC 480
QY 959 CTGAGAGAGCGCTGSCCAAGGTGAGAGAGAACTCACCCTCAAGGTGCTGAGAGTGGC 1018
Db 481 CTGAGAGAGCGCTGSCCAAGGTGAGAGAGAACTCACCCTCAAGGTGCTGAGAGTGGC 540
QY 1019 TGGATGAATTGGAGAGATGATGCTGCTGCTCACAATGCCCCGCTTCCGCAATTGA-GGAG 1077
Db 541 TGGATGAATTGGAGAGATGATGCTGCTGCTCACAATGCCCCGCTTCCGCAATTGAGGAGC 600
QY 1078 GGCCTTCAGTTGAGAGAGCAG-CTGCAGAGACATGGGCTTGTGATCTGTTGAGCCCT 1134
Db 601 GCTTCAGTTGAGAGAGCCGCTGCTGAGACATGGGCTTGTGATCTGTTGAGCCCT 658

Search completed: June 27, 2003, 00:05:50
Job time : 1904 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 26, 2003, 16:14:37 ; Search time 3598 Seconds
(without alignments)
11283.606 Million cell updates/sec

Title: US-09-828-592-6
Perfect score: 1395
Sequence: 1 atgtatccatgcatgcatag.....ccaaccttggttaagtaa 1395

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl:*

- 1: gb_ba:*
- 2: gb_hcg:*
- 3: gb_in:*
- 4: gb_om:*
- 5: gb_ov:*
- 6: gb_pat:*
- 7: gb_ph:*
- 8: gb_pl:*
- 9: gb_pr:*
- 10: gb_ro:*
- 11: gb_sts:*
- 12: gb_sy:*
- 13: gb_un:*
- 14: gb_vi:*
- 15: em_da:*
- 16: em_fun:*
- 17: em_hum:*
- 18: em_in:*
- 19: em_mu:*
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- 21: em_or:*
- 22: em_ov:*
- 23: em_pat:*
- 24: em_ph:*
- 25: em_pl:*
- 26: em_ro:*
- 27: em_sts:*
- 28: em_un:*
- 29: em_vi:*
- 30: em_hcg_hum:*
- 31: em_hcg_inv:*
- 32: em_hcg_other:*
- 33: em_hcg_mus:*
- 34: em_hcg_pln:*
- 35: em_hcg_rtd:*
- 36: em_hcg_mam:*
- 37: em_hcg_vrt:*
- 38: em_ay:*
- 39: em_htgo_hum:*
- 40: em_htgo_mus:*
- 41: em_htgo_other:*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|--------|-------------|--------|-------|-------------|
| 1 | 1395 | 100.0 | 1489 | 6 | A22203 |
| 2 | 1391.8 | 99.8 | 1599 | 6 | A06100 |
| 3 | 1391.8 | 99.8 | 1599 | 6 | 103102 |
| 4 | 1391.8 | 99.8 | 1600 | 6 | E00116 |
| 5 | 1391.8 | 99.8 | 1794 | 17 | AF130100 |
| 6 | 1390.2 | 99.7 | 1599 | 6 | 102335 |
| 7 | 1388.6 | 99.5 | 1395 | 6 | 112223 |
| 8 | 1385.6 | 99.3 | 1392 | 6 | E06109 |
| 9 | 1375.6 | 98.6 | 1467 | 9 | HUMAT11V |
| 10 | 1114.8 | 79.9 | 1751 | 4 | OMA111 |
| 11 | 1063.6 | 76.2 | 1509 | 10 | S47225 |
| 12 | 1063.6 | 76.2 | 1672 | 10 | BC019447 |
| 13 | 971.6 | 69.6 | 1527 | 10 | AB027228 |
| 14 | 702.2 | 50.3 | 1362 | 5 | AF411692 |
| 15 | 690 | 49.5 | 1542 | 5 | AF335570 |
| 16 | 675 | 48.4 | 1755 | 5 | AF411691 |
| 17 | 633.8 | 45.4 | 1272 | 5 | S79838 |
| 18 | 569.4 | 40.8 | 1371 | 5 | AF411693 |
| 19 | 564.2 | 40.4 | 988 | 5 | BC022309 |
| 20 | 562.2 | 40.3 | 1547 | 5 | AS0252153 |
| 21 | 412 | 29.5 | 572 | 4 | AF281653 |
| 22 | 401.2 | 28.8 | 14206 | 9 | HSAT3 |
| 23 | 401.2 | 28.8 | 62125 | 9 | AL691487 |
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| 26 | 398 | 28.5 | 16330 | 9 | AF386078 |
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| 28 | 372 | 26.7 | 604 | 9 | HUMATH3U2 |
| 29 | 359.2 | 25.7 | 385 | 9 | HUMATH3X3 |
| 30 | 326.4 | 23.4 | 20993 | 10 | AB043785 |
| 31 | 276.4 | 19.8 | 311 | 9 | HSAT3G1 |
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| 33 | 220.8 | 15.8 | 398 | 9 | HUMATH3A1 |
| 34 | 220.8 | 15.8 | 644 | 9 | HUMATH3U3 |
| 35 | 217.8 | 15.6 | 1256 | 5 | AF006495 |
| 36 | 191.8 | 13.7 | 2490 | 5 | AB026832 |
| 37 | 182.4 | 13.1 | 90216 | 2 | AC113837 |
| 38 | 179.8 | 12.9 | 238 | 9 | HUMATH3A3 |
| 39 | 179 | 12.8 | 230 | 9 | HSAT3G2 |
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| 41 | 178.2 | 12.8 | 324 | 9 | HUMATH3U7 |
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| 43 | 144.4 | 10.4 | 469 | 9 | HUMATH3A2 |
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| 45 | 144.4 | 10.4 | 80780 | 2 | AC020777 |

ALIGNMENTS

RESULT 1

LOCUS A22203 1489 bp mRNA linear PAT 21-JUL-1994

DEFINITION Antithrombin III.

ACCESSION A22203

VERSION A22203.1 GI:583740

KEYWORDS

ORGANISM

SOURCE

FEATURES

source

gene

Location/Qualifiers

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Matches 1395; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2

LOCUS A06100 1599 bp mRNA linear PAT 08-JUL-1993
DEFINITION Synthetic human antithrombin III mRNA.
ACCESSION A06100
VERSION A06100.1 GI:412722
KEYWORDS

SOURCE

ORGANISM synthetic construct.
synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 1599)
Bock,S.C. and Lawn,R.M.

AUTHORS

TITLE Human antithrombin III. DNA sequences thereof, expression vehicles and cloning vectors containing such sequences and cell cultures transformed thereby, a process for expressing human antithrombin III, and pharmaceutical compositions comprising it
Patent: EP 0090505-A 5 05-OCT-1983;
GENENTECH, INC

JOURNAL

FEATURES

source

1..1599 location/Qualifiers
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Best Local Similarity 99.9%; Pred. No. 0;
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DB      241 ACAGCAAGCCGCGGGACATTTCCCATGATGTCATGTCATTTACCGCTCCCGGAGAAG 300
QY      181 AAGCAACTGAGAGATGAGAGGCTCAGAACAGATCCCGGAGGCCACCAACCGCGCTGC 240
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 VERSION 103102.1 GI:268574
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 1599)
 AUTHORS Bock,S.C. and Lawn,R.M.
 TITLE Human antithrombin III
 JOURNAL Patent: US 4632981-A 1 30-DEC-1986;
 Genentech, Inc.; South San Francisco, CA
 FEATURES
 source 1..1599
 location/Qualifiers
 BASE COUNT 421 a 409 c 375 g 394 t
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 Best Local Similarity 99.9%; Pred. No. 0;
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 ACCESSION E00116 GI:2168417
 VERSION E00116.1
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 SOURCE Homo sapiens.
 ORGANISM Homo sapiens
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 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 1600)
 AUTHORS Suizuan,K.B. and Richiyoado,E.R.
 TITLE HUMAN ANTITHROMBOTIC III
 JOURNAL Patent: JP 1983162529-A 1 27-SEP-1983;
 GENENTECH INC

COMMENT
 OS human
 PN JP 1983162529-A/1
 PD 27-SEP-1983
 PF 03-MAR-1983 JP 1983033900
 PR 03-MAR-1982 GB 82 8206262, 30-JUL-1982 US 82 403600 PI
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 CC hypothetical: No;
 CC anti-sense: No;
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 BASE COUNT 422 a 409 c 375 g 394 t
 ORIGIN

Query Match 99.8%; Score 1391.8; DB 6; Length 1600;
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 Matches 1393; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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Oy 1201 CATAGGCAATTTCTTGAGGTAAATGAGAAAGCAGTGAAGCAGTGCAGATCCGCTGTT 1260
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Oy 1261 GTGATTTCTGAGCCGCTGCTAAACCCCAAGAGGTGACTTTCAAGGCCCAAGGCCCTTTC 1320
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Oy 1321 CTGCTTTTATTAAGAAAGTTTCTCTGAACACTTATCTTCATGAGGCGAGTACGCCAAC 1380
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Db 1501 CCTGTGTTAAGTAA 1515

RESULT 5
AF130100 standard; RNA; HUM; 1794 BP.
XX AF130100,
XX AC AF130100,
XX SV AF130100.1
XX 03-DEC-2000 (Rel. 66, Created)
DT 09-MAY-2001 (Rel. 67, Last updated, Version 2)
DE Homo sapiens clone FLB1413 PRO0309 mRNA, complete cds.
XX
XX Homo sapiens (human)
XX OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
XX OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
XX
XX [1]
XX RN 1-1794
XX RP Zhang C., Yu Y., Zhang S., Wei H., Bi J., Zhou G., Dong C., Zai Y., Xu W.,
XX RA Gao F., Liu M., He F.;
XX RT "Functional prediction of the coding sequences of 75 new genes deduced by
XX RL analysis of cDNA clones from human fetal liver";
XX
XX [2]
XX RN 1-1794
XX RP Zhang C., Yu Y., Zhang S., Wei H., Bi J., Zhou G., Dong C., Zai Y., Xu W.,
XX RA Gao F., Liu M., He F.;
XX RT Submitted (23-FEB-1999) to the EMBL/GenBank/DBJ databases.
XX RL Department of Experimental Hematology, Institute of Radiation Medicine,
XX RL Beijing Taiding Road 27, Beijing, Beijing 100850, P. R. China
XX
XX DR SWISS-PROT; P01008; ANT3_HUMAN.
XX
XX Key Location/Qualifiers
FH 1. 1794
FH source /db_xref="taxon:9606"
FH FT /organism="Homo sapiens"
FH FT /clone="FLB1413"
FH FT /rissue_type="liver"
FH FT /dev_stage="fetus"
FH FT repeat_region 16..137
FH FT /rpt_family="Alu"
FH FT /rpt_type=DISPERSED
FH FT 234..1628
FH FT /codon_start=1
FH FT /db_xref="SWISS-PROT:P01008"
FH FT /evidence=NOT_EXPERIMENTAL
FH FT /note="predicted protein of H00309"
FH FT /product="PRO0309"

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FT      /protein_id="AAG35525.1"
FT      /translation="MYSNVIQVTSKRVYLLSLIFPMDCVTHGSPVDICTAKPR
FT      DIIPNMCYRSEPKATEDEBSEOKIPATNRNWELEKSNRSPATTEYOHLSKND
FT      NNIIFSPISITAFAMTKLACNDLQOEVEFKPDITSEKSDIDHFFKAMICRLY
FT      RANKSKSLVSNARLFGDSLFPENETIODISLVGAKIOPIDFKENASQSAIINKW
FT      SKTEGRITDVI PSEAINELIYVIVNTIYFKGIIMSKREI.PYKADGSCSA
FT      SMYQDGRKRRYRVAGCTOVLPLPKGDITDWTLLIPREKSLAKREKLLPVELOEML
FT      DELSEMLVVMHPRFRIEDGFSLKEQLQMDGLVDFSPKSKLPGIIVAGRDLIVSDA
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XX
SQ      Sequence 1794 bp; 540 A; 429 C; 420 G; 405 T; 0 other;

Query Match      99.8%; Score 1391.8; DB 17; Length 1794;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1393; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1  ATGTATTCCAATGTGATAGGAAGTAACTGTAACCTCTGGAAGAAAGAGGTTATCTTTGTC 60
DB      234  ATGTATTCCAATGTGATAGGAAGTAACTGTAACCTCTGGAAGAAAGAGGTTATCTTTGTC 293
QY      61  TTGCTGCTAATGCTGCTTCTGGAGCTGCGTGAACCTGTACAGGAGCCCTGTGACATCTGC 120
DB      294  TTGCTGCTAATGCTGCTTCTGGAGCTGCGTGAACCTGTCAAGGAGCCCTGTGACATCTGC 353
QY      121  ACAGCCAAAGCCGCGGACATTTCCCATGATATCCCATGTGATTCGCTCCCGGAGAA 180
DB      354  ACAGCCAAAGCCGCGGACATTTCCCATGATATCCCATGTGATTCGCTCCCGGAGAA 413
QY      181  AAGGCAACTGAGGATGAGGAGCTGAGAACAGAAATCCGAGAGCCCAACCGGCGTGC 240
DB      414  AAGGCAACTGAGGATGAGGAGCTGAGAACAGAAATCCGAGAGCCCAACCGGCGTGC 473
QY      241  TGGGAATGTCGCAAGGCAATTCGCTTTGCTACCACTTTCTATGAGACCTGGAGAT 300
DB      474  TGGGAATGTCGCAAGGCAATTCGCTTTGCTACCACTTTCTATGAGACCTGGAGAT 533
QY      301  TCCAAAGATGACATGATTAATATTTCTGTCAACCCCTGATGATCTTCACGCGCTTTGCT 360
DB      534  TCCAAAGATGACATGATTAATATTTCTGTCAACCCCTGATGATCTTCACGCGCTTTGCT 593
QY      361  ATGACCAAGCTGGGTGCTGTATGACACCTCCAGAACATGATGAGGATTTAGATT 420
DB      594  ATGACCAAGCTGGGTGCTGTATGACACCTCCAGAACATGATGAGGATTTAGATT 653
QY      421  GACACCATATCTGAGAAAACATCTGATCAGATCACTTCTTTGCCAACTGAACTGC 480
DB      654  GACACCATATCTGAGAAAACATCTGATCAGATCACTTCTTTGCCAACTGAACTGC 713
QY      481  CGACTCTATGAGAAAACCAATCTCTCAAGTTAGTATCAGCCATGCGCTTTTGA 540
DB      714  CGACTCTATGAGAAAACCAATCTCTCAAGTTAGTATCAGCCATGCGCTTTTGA 773
QY      541  GACAAATCCCTTACCTTCAATGAGACCTTACAGAGATCAGTATGATGATGAGGC 600
DB      774  GACAAATCCCTTACCTTCAATGAGACCTTACAGAGATCAGTATGATGATGAGGC 833
QY      601  AAGCTCAGCCCTCTGACCTTCAAGAAAATGACAGCAATCCAGACGCGCATCAAAA 660
DB      834  AAGCTCAGCCCTCTGACCTTCAAGAAAATGACAGCAATCCAGACGCGCATCAAAA 893
QY      661  TGGGTCTCAATTAAGACCGAAGCCGATATCAGATGATCTTCTCTGGAAGCCATCAAT 720
DB      894  TGGGTCTCAATTAAGACCGAAGCCGATATCAGATGATCTTCTCTGGAAGCCATCAAT 953
QY      721  GAGCTACTGTTCTGGGTGCTGTTAACACCATTTACTTCAAGGCGCTGTGGAAGTAAAG 780
DB      954  GAGCTACTGTTCTGGGTGCTGTTAACACCATTTACTTCAAGGCGCTGTGGAAGTAAAG 1013
QY      781  TTCAGCCCTGAGAACCAAGGAAGAACTGTTTCAAGAGCTGATGAGAGTGTGTTCA 840
DB      1014  TTCAGCCCTGAGAACCAAGGAAGAACTGTTTCAAGAGCTGATGAGAGTGTGTTCA 1073

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QY      841  GCATCTATGATGTATACAGGAAGCAAGTCCGTTATCCGCCCGCTGAGGACCCAG 900
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DB      1194  GAGAAAGCTCGGCCAAGGTGAGAAAGAACTCACCCAGAGGTGCTCAGAGTGGCTG 1253
QY      1021  GATGAATTGAGAGAAATATGCTGTGTCACATGCCCGCTTCCGATGAGAGACGC 1080
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QY      1081  TTCAGTTGAAGAGACAGCTGCAACATGAGGCGCTTTCGATCTGTTCAAGCCCTGAAAAG 1140
DB      1314  TTCAGTTGAAGAGACAGCTGCAACATGAGGCGCTTTCGATCTGTTCAAGCCCTGAAAAG 1373
QY      1141  TCCAAATCCCAAGTATTGTTGACAGAGCCGAGATGACCTCTATGTCTCAGATGCATTC 1200
DB      1374  TCCAAATCCCAAGTATTGTTGACAGAGCCGAGATGACCTCTATGTCTCAGATGCATTC 1433
QY      1201  CATTAAGCATTTCTTGAGTAAATTAAGAAGGCAATGAGCAGCTGCAAGTACCGCTGT 1260
DB      1434  CATTAAGCATTTCTTGAGTAAATTAAGAAGGCAATGAGCAGCTGCAAGTACCGCTGT 1493
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DB      1494  GTGATTTGCTGGCGCTTGCCTAAACCCCAACAGGGTGACTTTCAAGGCCCAACAGGCTTTC 1553
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DB      1554  CTGCTTTTATTAAGAAAGTTCCTCTGAACATATATCTTCAATGAGGACAGTACCAAC 1613
QY      1381  CCTTGCTTAAAGTAA 1395
DB      1614  CCTTGCTTAAAGTAA 1628

RESULT 6
LOCUS      102335 1599 bp ss-DNA linear PAT 18-MAY-1993
DEFINITION Sequence 1 from Patent US 4517294.
ACCESSION 102335
VERSION 102335.1 GI:268048
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1599)
AUTHORS Bock,S.C. and Lawn,R.M.
TITLE Human antithrombin III
JOURNAL Patent: US 4517294-A 1 14-MAY-1985;
Genentech, Inc.; South San Francisco, CA
FEATURES
source 1..1599
/organism="unknown"
BASE COUNT 421 a 408 c 375 g 395 t
ORIGIN
Query Match 99.7%; Score 1390.2; DB 6; Length 1599;
Best Local Similarity 99.8%; Pred. No. 0;
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QY      1  ATGTATTCCAATGTGATAGGAAGTAACTGTAACCTCTGGAAGAAAGAGGTTATCTTTGTC 60
DB      121  ATGTATTCCAATGTGATAGGAAGTAACTGTAACCTCTGGAAGAAAGAGGTTATCTTTGTC 180
QY      61  TTGCTGCTAATGCTGCTTCTGGAGCTGCGTGAACCTGTACAGGAGCCCTGTGACATCTGC 120
DB      181  TTGCTGCTAATGCTGCTTCTGGAGCTGCGTGAACCTGTACAGGAGCCCTGTGACATCTGC 240

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| | | | |
|----|------|--|------|
| Qy | 121 | ACAGCAGACCGGGGACATTTCCCATGAAATCCCATGTGCATTTACCGCTCCCGGGAGAG | 180 |
| Db | 241 | ACAGCGAAGCCGGGGACATTTCCCATGAAATCCCATGTGCATTTACCGCTCCCGGGAGAG | 300 |
| Qy | 181 | AAGGCAACTGAGATGAGGGCTCAGAAAGAAATCCCGAGGGCCACAAACCGGGTGTG | 240 |
| Db | 301 | AAGGCAACTGAGATGAGGGCTCAGAAAGAAATCCCGAGGGCCACCAACCGGGTGTG | 360 |
| Qy | 241 | TGGGAATCTGTCCAAAGGCCAATTTCCCGCTTTGCTACCACTTTCTATCAGCACTGGCAAT | 300 |
| Db | 361 | TGGGAATCTGTCCAAAGGCCAATTTCCCGCTTTGCTACCACTTTCTATCAGCACTGGCAAT | 420 |
| Qy | 301 | TCCAAAGATGACAAATGATACATTTTCCGTGTACACCCCTGAGATCTCCAGGGCTTTGCT | 360 |
| Db | 421 | TCCAAAGATGACAAATGATACATTTTCCGTGTACACCCCTGAGATCTCCAGGGCTTTGCT | 480 |
| Qy | 361 | ATGACCAAGCTGGGTGCTGTATGACACCTCTCAGCAACTGATGAGAGTATTTAAGTTT | 420 |
| Db | 481 | ATGACCAAGCTGGGTGCTGTATGACACCTCTCAGCAACTGATGAGAGTATTTAAGTTT | 540 |
| Qy | 421 | GACACCAATCTGAGAAAACATCTGATGAGATCCACTTCTTGTGCCAAATGAACTGC | 480 |
| Db | 541 | GACACCAATCTGAGAAAACATCTGATGAGATCCACTTCTTGTGCCAAATGAACTGC | 600 |
| Qy | 481 | CGACTCTATCGAAAAGCCAAACAAATCTTCAAGTTAGTATCAGCCAAATCGCTTTTGTGA | 540 |
| Db | 601 | CGACTCTATCGAAAAGCCAAACAAATCTTCAAGTTAGTATCAGCCAAATCGCTTTTGTGA | 660 |
| Qy | 541 | GACCAATCCCTTACCTTCAATGAGACTTACAGGACATCATGTAAGTGTATATGAGGC | 600 |
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| Qy | 601 | AAGCTCCAGCCCTGAGACTTCAAGGAAATGACAGACATCCAGAGCGGCATCAACAA | 660 |
| Db | 721 | AAGCTCCAGCCCTGAGACTTCAAGGAAATGACAGACATCCAGAGCGGCATCAACAA | 780 |
| Qy | 661 | TGGGTGTCCAATTAAGACCGAAGGCCGAATCACCGATGTCAATTCCTCGAAGCCATCAAT | 720 |
| Db | 781 | TGGGTGTCCAATTAAGACCGAAGGCCGAATCACCGATGTCAATTCCTCGAAGCCATCAAT | 840 |
| Qy | 721 | GAGCTCACTGTTCTGSGTCTGTTTAAACACATTTTACTTCAAGGGCTGTGAAAGTCAAG | 780 |
| Db | 841 | GAGCTCACTGTTCTGSGTCTGTTTAAACACATTTTACTTCAAGGGCTGTGAAAGTCAAG | 900 |
| Qy | 781 | TTTCAGCCCTTGAGAACACAAGAGAGAACTGTTCTAACAAGGCTGATGAGAGTCTGTCA | 840 |
| Db | 901 | TTTCAGCCCTTGAGAACACAAGAGAGAACTGTTCTAACAAGGCTGATGAGAGTCTGTCA | 960 |
| Qy | 841 | GCATCTATGATGTACAGGAAGGCAAGTTCCGTTATCGGCGCTGAGCTGAAAGCCACAG | 900 |
| Db | 961 | GCATCTATGATGTACAGGAAGGCAAGTTCCGTTATCGGCGCTGAGCTGAAAGCCACAG | 1020 |
| Qy | 901 | GTGCTTGAGTTGGCCCTTCAAAGGTATGACATCACATGSGTCTCATCTTGGCCAAAGCT | 960 |
| Db | 1021 | GTGCTTGAGTTGGCCCTTCAAAGGTATGACATCACATGSGTCTCATCTTGGCCAAAGCT | 1080 |
| Qy | 961 | GAGAAAGACCTGGCCCAAGGTGAGAAAGAACTCACCCAGAGAGTCTGCAGAGATGGCTG | 1020 |
| Db | 1081 | GAGAAAGACCTGGCCCAAGGTGAGAAAGAACTCACCCAGAGAGTCTGCAGAGATGGCTG | 1140 |
| Qy | 1021 | GATGAATTTGGAGAGATGATGTTGTTGTGTCCCATGCCCCGTTTCCGATTTGAGACGGC | 1080 |
| Db | 1141 | GATGAATTTGGAGAGATGATGTTGTTGTGTCCCATGCCCCGTTTCCGATTTGAGACGGC | 1200 |
| Qy | 1081 | TTTCAGTTTGAAGAGACAGCTGCACAACATGGGCTTGTGATCTGTTTCAGCCCTGAAAAG | 1140 |
| Db | 1201 | TTTCAGTTTGAAGAGACAGCTGCACAACATGGGCTTGTGATCTGTTTCAGCCCTGAAAAG | 1260 |
| Qy | 1141 | TTCCAAATCTCCAGGATATTGTTGACAGAGGCCGAGATGACCTTATATGTCTCAGATCATTC | 1200 |
| Db | 1261 | TTCCAAATCTCCAGGATATTGTTGACAGAGGCCGAGATGACCTTATATGTCTCAGATCATTC | 1320 |

| | | | |
|----------------------------|--|---|----------------------------|
| QY | 1201 | CATAGAGCATTTCTTGAGGTAAATGAGAGGACGTGAAGCGCTGCAAGTACCGTGT | 1260 |
| Db | 1321 | CATAGGCAATTTCTTGAGGTAAATGAGAGGACGTGAAGCGCTGCAAGTACCGTGT | 1380 |
| QY | 1261 | GTGATGTGCGCGCTTGCTAAACCCCAACGAGGTGACTTTCAAGGCCAAGGCTTTC | 1320 |
| Db | 1381 | GTGATGTGCGCGCTTGCTAAACCCCAACGAGGTGACTTTCAAGGCCAAGGCTTTC | 1440 |
| QY | 1321 | CTGGTTTTTAAAGAGAAAGTTCCCTGTGAACACTATTTATCTTCAATGGGCAAGTACCAAC | 1380 |
| Db | 1441 | CTGGTTTTTAAAGAGAAAGTTCCCTGTGAACACTATTTATCTTCAATGGGCAAGTACCAAC | 1500 |
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| Db | 1501 | CCTGTGTAAAGTAA 1515 | |
| RESULT 7. | | | |
| LOCUS | 112223 | 1395 bp | DNA linear PAT 26-JUL-1995 |
| DEFINITION | Sequence 1 from patent US 5420252. | | |
| ACCESSION | 112223 | | |
| VERSION | 112223.1 | GI:909721. | |
| KEYWORDS | | | |
| SOURCE | Unknown. | | |
| ORGANISM | Unknown. | | |
| REFERENCE | Unclassified. | | |
| AUTHORS | 1 (bases 1 to 1395) | | |
| | Kato,H., Yoshitake,S., Suzuki,S., Suzuki,N., Seto,T., Nagaoka,N. | | |
| | and Mizui,Y. | | |
| TITLE | Human antithrombin III mutants | | |
| JOURNAL | Patent: US 5420252-A 1 30-MAY-1995; | | |
| FEATURES | Location/Qualifiers | | |
| source | 1..1395 | | |
| | /organism="unknown" | | |
| BASE COUNT | 368 a 353 c 343 g 331 t | | |
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| Query Match | 99.5%; Score 138.6; DB 6; Length 1395; | | |
| Best Local Similarity | 99.7%; Pred. No. 0; | | |
| Matches 1391; Conservative | 0; Mismatches 4; Indels 0; Gaps 0; | | |
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| Db | 1 | ATGATATTCCAATGTGATGGAACGTGTAACCTCTGTGAAAAAGAAAGTTTATCTTTGTCC | 60 |
| QY | 61 | TTGCGTCATATGGCTTCTGTGGACGTGGGTGACCTGTCACGGAGGCCGTGAGACATCTGC | 120 |
| Db | 61 | TTGCGTCATATGGCTTCTGTGGACGTGGGTGACCTGTCACGGAGGCCGTGAGACATCTGC | 120 |
| QY | 121 | ACAGCCAAGCCGCGGAGACATTCGCCATGATCCCATGTGTCATTCACGCTCCCGGAGAA | 180 |
| Db | 121 | ACAGCCAAGCCGCGGAGACATTCGCCATGATCCCATGTGTCATTCACGCTCCCGGAGAA | 180 |
| QY | 181 | AAGCAACTGAGATGAGAGGCTCAGAACAGAAATCCCGAGGCCAACCAACCGCGTGTCT | 240 |
| Db | 181 | AAGCAACTGAGATGAGAGGCTCAGAACAGAAATCCCGAGGCCAACCAACCGCGTGTCT | 240 |
| QY | 241 | TGGGAACGTGCCAAGGCCAATTCGCCGCTTTCCTACACATTTCTATACGACACTGGCAAT | 300 |
| Db | 241 | TGGGAACGTGCCAAGGCCAATTCGCCGCTTTCCTACACATTTCTATACGACACTGGCAAT | 300 |
| QY | 301 | TCCAAAGATGACAAATGATTAATTTTCTGTACACCCCTGAGTATCTCACGAGCTTTTCT | 360 |
| Db | 301 | TCCAAAGATGACAAATGATTAATTTTCTGTGTACACCCCTGAGTATCTCACGAGCTTTTCT | 360 |
| QY | 361 | ATGACCAAGCTGGGTGCTGTATGACACCTTCAGCAACTGATGAGAGTAAATTAAGTTT | 420 |
| Db | 361 | ATGACCAAGCTGGGTGCTGTATGACACCTTCAGCAACTGATGAGAGTAAATTAAGTTT | 420 |
| QY | 421 | GACACCAATCTTGAGAAAACATCTGATCAATTCACATTTCTTTTCCAACTGAATCTGC | 480 |
| Db | 421 | GACACCAATCTTGAGAAAACATCTGATCAATTCACATTTCTTTTCCAACTGAATCTGC | 480 |

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|----|------|--|------|
| Db | 481 | CGAGCTCTATCGAAGAACCAAAATCTCCCAAGTTAGTATCAGCCAAATGCGCTTTTGG | 540 |
| Qy | 541 | GACAAATCCCTTACCTTCAATGAGACTTACACAGACATCAGTGGATTATATGAGCC | 600 |
| Db | 541 | GACAAATCCCTTACCTTCAATGAGACTTACACAGACATCAGTGGATTATATGAGCC | 600 |
| Qy | 601 | AAGCTCCAGCCCTCGAGCTTCAAGGAAATGAGAGCAATCCAGAGCCGCTTCAACAA | 660 |
| Db | 601 | AAGCTCCAGCCCTCGAGCTTCAAGGAAATGAGAGCAATCCAGAGCCGCTTCAACAA | 660 |
| Qy | 661 | TGGGTGTCCTAATAGACCCAGAGCCGATCACCAGATGTCATTCCTCCGGAAGCCATCAAT | 720 |
| Db | 661 | TGGGTGTCCTAATAGACCCAGAGCCGATCACCAGATGTCATTCCTCCGGAAGCCATCAAT | 720 |
| Qy | 721 | GAGCTCACTGTTCTGTGCTGTTAACAACATTTTACTTCAAGAGGCTGTGGAAGTCAAG | 780 |
| Db | 721 | GAGCTCACTGTTCTGTGCTGTTAACAACATTTTACTTCAAGAGGCTGTGGAAGTCAAG | 780 |
| Qy | 781 | TTCAAGCCCTGGAACACAAAGGAAGAACTGTTCTTCAAGAGCTGATGAGAGTCTGTCTCA | 840 |
| Db | 781 | TTCAAGCCCTGGAACACAAAGGAAGAACTGTTCTTCAAGAGCTGATGAGAGTCTGTCTCA | 840 |
| Qy | 841 | GCATCTATGATGTATACAGGAAGGCAAGTTCCGTTATCGGCGCGGTGGCTGAAGGACCCAG | 900 |
| Db | 841 | GCATCTATGATGTATACAGGAAGGCAAGTTCCGTTATCGGCGCGGTGGCTGAAGGACCCAG | 900 |
| Qy | 901 | GTCCTTGAAGTTGCCCCCTTCAAAAGTGATGACATCACCATGTCCTCATCTTGGCCAAAGCT | 960 |
| Db | 901 | GTCCTTGAAGTTGCCCCCTTCAAAAGTGATGACATCACCATGTCCTCATCTTGGCCAAAGCT | 960 |
| Qy | 961 | GAGAAAGACCTCGGCCAAGTGGAGAAAGAACTCACCCAGAGTGTCTGAGAGATGGCTG | 1020 |
| Db | 961 | GAGAAAGACCTCGGCCAAGTGGAGAAAGAACTCACCCAGAGTGTCTGAGAGATGGCTG | 1020 |
| Qy | 1021 | GATGAATTTGAGAGAGATGATGCTGTGTTGTCACATGCCCCGCTTCGCAATTGAGAGACGGC | 1080 |
| Db | 1021 | GATGAATTTGAGAGAGATGATGCTGTGTTGTCACATGCCCCGCTTCGCAATTGAGAGACGGC | 1080 |
| Qy | 1081 | TTCAAGTTTGAAGAGACAGCTGCAAGACATGGGCTTGTTCGATCTGTTCAAGCCCTGAAGA | 1140 |
| Db | 1081 | TTCAAGTTTGAAGAGACAGCTGCAAGACATGGGCTTGTTCGATCTGTTCAAGCCCTGAAGA | 1140 |
| Qy | 1141 | TTCAAACTTCCAGAGTATTTGTTSCAGAGAGCCGAGATGACCTTATATGTTCTCAGATGCATTC | 1200 |
| Db | 1141 | TTCAAACTTCCAGAGTATTTGTTSCAGAGAGCCGAGATGACCTTATATGTTCTCAGATGCATTC | 1200 |
| Qy | 1201 | CATAAGGATTTCTTGAGGTAAATGAAGAGCAATGAAGCAAGCTGCAAGTACCGCTGT | 1260 |
| Db | 1201 | CATAAGGATTTCTTGAGGTAAATGAAGAGCAATGAAGCAAGCTGCAAGTACCGCTGT | 1260 |
| Qy | 1261 | GTCATTCGTGCGCGTTCCCTAAACCCCAACAGGAGTGACTTTCAAGGCCAAGGCGCTTTC | 1320 |
| Db | 1261 | GTCATTCGTGCGCGTTCCCTAAACCCCAACAGGAGTGACTTTCAAGGCCAAGGCGCTTTC | 1320 |
| Qy | 1321 | CTGGTTTTTATPAGAGAAATTCTCTGAACACTATTTATCTTATGAGGCGAGATGACCAAC | 1380 |
| Db | 1321 | CTGGTTTTTATPAGAGAAATTCTCTGAACACTATTTATCTTATGAGGCGAGATGACCAAC | 1380 |
| Qy | 1381 | CCTGTGTGTTAAG 1392 | |
| Db | 1381 | CCTGTGTGTTAAG 1392 | |

| RESULT 9 | HUMATITIV |
|------------|---|
| LOCUS | HUMATITIV 1467 bp mRNA linear PRI 07-FEB-1993 |
| DEFINITION | Human mRNA for antithrombin III variant, complete cds. |
| ACCESSION | D29832 |
| VERSION | D29832.1 GI:576553 |
| KEYWORDS | AT-III; antithrombin III. |
| SOURCE | Homo sapiens (individual isolate AT-III Kyoto) cDNA to mRNA, clone pK16c. |
| ORGANISM | Homo sapiens |

| REFERENCE
AUTHORS
TITLE | JOURNAL |
|---|--|
| Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (sites) Teuji, H., Takada, O., Nakagawa, M., Tanaka, S. and Hashimoto-Gotoh, T. Hereditary antichromom III deficiency: identification of an arginine-406 to methionine point mutation near protease reactive site (in) Yoshida, T.O. and Wilson, J.M. (Eds.), MOLECULAR APPROACHES TO THE STUDY AND TREATMENT OF HUMAN DISEASES: 51-55; Elsevier Science (1992) 2 (bases 1 to 1467) Hashimoto-Gotoh, T. Unpublished | |
| REFERENCE
AUTHORS
JOURNAL
FEATURES
source | Location/Qualifiers |
| CDS | 1. 1467 /organism="Homo sapiens" /db_xref="taxon:9606" 22. 1419 /note="Wild type AT-III has 'g' instead of 'c' at position 1337 nt. Also amino acid residue changes from Met to Arg at position 406 aa in wild type AT-III." /codon_start=1 /product="antithrombin III (AT-III) variant" /protein_id="BAA06212.1" /db_xref="GI:576554" /translation="MYSNVIGTVTSGRKYLLSLILIGMDCVTCGSPVDICTAKP RDIIPNMCITRSPEKKATEDEGSEOKI PATNRRVRLSKASRPATFYOHIAOS KNDINDIPLSPISLSTAPMTKLGACNDTLQOLMEVVKPDTISKTSKDPKHAIAK INRYRANKSKSVASRRLPGDGSITFNEYNTDSELVYAKIOLPDKHGEOSRPA IKNVRSKRTSGRTIDVYPSERINELTYLVYNTITFYGLMSKRSPEPTKRELFPKAD GESGSASMTYDEGKFRFRVAEGQVLELPKGGDITMVALLPKPSKLVKVELLP EVLQVLEDFELKEMMLVHMPRFRIEDFSLKEQLQDGLVDLSPSPSKIPGIYAEGR DDIIVSDAFKFAFLFVNEEGSEAASTAIVIAVAGSLNPNRVTFKAMPFLVFIREVLP NTIIFMGRVANPCVK" |
| BASE COUNT | 381 a 375 c 364 g 347 t |
| ORIGIN | |
| Query Match | 98.6%; Score 1375.6; DB 9; Length 1467; |
| Best Local Similarity | 99.5%; Pred. No. 0; |
| Matches 1391; Conservative | 0; Mismatches 4; Indels 3; Gaps 1; |
| QY | 1 ATGTAATTCGAATGTGATAGGAACCTGTAACCTCTGGAAAAAGAAAGTTATCTTTGTCC 60 |
| DB | 22 ATGTAATTCGAATGTGATAGGAACCTGTAACCTCTGGAAAAAGAAAGTTATCTTTGTCC 81 |
| QY | 61 TTGTCGTCAATTTGGCTCTCTGGGACCTGGTACCTGTACACGGGAGCCCTGTGGAATCTGC 120 |
| DB | 82 TTGTCGTCAATTTGGCTCTCTGGGACCTGGTACCTGTACACGGGAGCCCTGTGGAATCTGC 141 |
| QY | 121 ACAGCCCAAGCCGCGGACATTTCCCATGAATCCCATGTGATTTACCGCTCCCGGAGAG 180 |
| DB | 142 ACAGCCCAAGCCGCGGACATTTCCCATGAATCCCATGTGATTTACCGCTCCCGGAGAG 201 |
| QY | 181 AAGGCAACTGAGATGAGGGCTCAGAA CAGAAATCCCGAGAGCCAC--CAACCGGCGT 237 |
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| QY | 238 GTCTGGGAACCTGTCCAAAGGCCAATTTCCCGCTTTGCTACCACTTTCTATCAGACCTGGCA 297 |
| DB | 262 GTCTGGGAACCTGTCCAAAGGCCAATTTCCCGCTTTGCTACCACTTTCTATCAGACCTGGCA 321 |
| QY | 298 GATTCCAAGAAATGACATGATATCATTTTCTCTGCACCCCTGAGTATCTCCAGCGGCTTTT 357 |
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| QY | 358 GCTATGACCAAGCTGGGTGCTGTATATGACACCCCTCAGACCACTGATGAGATATTTAAG 417 |
| DB | 382 GCTATGACCAAGCTGGGTGCTGTATATGACACCCCTCAGACCACTGATGAGATATTTAAG 441 |
| QY | 418 TTGTGACACCATATTTGAGAAAAACATCTGATCATCATCTTTCTTTTGGCAACTGAC 477 |
| DB | 442 TTGTGACACCATATTTGAGAAAAACATCTGATCATCATCTTTCTTTTGGCAACTGAC 501 |

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RESULT 10
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 DEFINITION X68287
 ACCESSION X68287.1 GI:1194
 VERSION antithrombin III; coagulation inhibitor.
 KEYWORDS

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SOURCE
ORGANISM
Ovis aries.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Bovidae; Caprine; Ovis.
REFERENCE
1 (bases 1 to 1751)
AUTHORS
Niessen,R.W.L.M.
TITLE
Direct Submission
JOURNAL
Submitted (08-SEP-1992) R.W.L.M. Niessen, Center for Hemostasis,
Thrombosis, Atherosclerosis & Inflammation Research, Academic
Medical Center, Meibergdreef 9, 1105 AZ Amsterdam, THE NETHERLANDS
2 (bases 1 to 1751)
AUTHORS
Niessen,R.W., Sturk,A., Hordijk,P.L., Michiels,F. and Peters,M.
TITLE
Sequence characterization of a sheep cDNA for antithrombin III
JOURNAL
Biochim. Biophys. Acta 1171 (2), 207-210 (1992)
PUBMED
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RESULT 11
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 ACCESSION S47225
 VERSION S47225.1 GI:258958
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 REFERENCE 1 (bases 1 to 1509)
 AUTHORS Wu, J. K., Sheffield, W. P., and Blajchman, M. A.
 TITLE Molecular cloning and cell-free expression of mouse antithrombin III
 JOURNAL Thromb. Haemost. 68 (3), 291-296 (1992)
 MEDLINE 93069082
 PUBMED 1440494
 REMARK GenBank staff at the National Library of Medicine created this entry [NCBI gibbon 117254] from the original journal article. This sequence comes from Fig. 2.
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RESULT 12
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 ACCESSION
 BC019447
 VERSION
 BC019447.1
 SOURCE
 house mouse.
 ORGANISM
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 1672)
 REFERENCE
 Strausberg, R.
 Direct Submission
 Submitted (19-DEC-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
 REMARK
 NIH-MGC Project URL: <http://mgc.nci.nih.gov>
 CONTACT
 Contact: MGC help desk
 Email: cgabs-remail.nih.gov
 Tissue Procurement: Jeffrey E. Green, M.D.
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILML)
 DNA Sequencing by: Baylor College of Medicine Human Genome Sequencing Center
 Center code: BCM-HGSC
 Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>
 Contact: amg@bcm.tmc.edu
 Guarante, P.H., Garcia, A.M., Lu, X., Huiyk, S.W., Hale, S.M., Yoon, V.S., Kowis, C.R., Lawrence, S., Martin, R.G., Muzny, D.M., Richards, S., Gibbs, R.A.
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/ILML at: <http://image.llnl.gov>
 Series: IRAX Plate: 41 Row: n Column: 23
 This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, similarity but not identity to protein.
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 Testudines; Cryptodira; Testudinoidea; Chelydridae; Chelydra.

REFERENCE
 AUTHORS Backovic,M. and Gettins,P.G.W.
 TITLE Insight into residues critical for antithrombin function from an expanded database of sequences that includes frog, turtle and ostrich antithrombins

JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 1362)
 AUTHORS Backovic,M. and Gettins,P.G.W.
 TITLE Direct Submission
 JOURNAL Submitted (21-AUG-2001) Biochemistry and Molecular Biology, University of Illinois at Chicago, 1819 W. Polk Street, CMW, M/C 536, Chicago, IL 60612, USA

FEATURES

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 REFERENCE
 1 (bases 1 to 1542)
 Mercalf, V.J., Brennan, S.O., George, P.M. and Chambers, G.K.
 The identification of liver-expressed genes from tuatara
 Unpublished
 2 (bases 1 to 1542)
 Mercalf, V.J., Brennan, S.O., George, P.M. and Chambers, G.K.
 Direct Submission
 Submitted (11-JUN-2001) Department of Pathology, Christchurch
 School of Medicine, University of Otago, PO Box 4345, Christchurch,
 New Zealand

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